



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 138939

TO: Terra Gibbs
Location: rem/2d10/2c18
Art Unit: 1635
Tuesday, December 07, 2004

Case Serial Number: 09/491063

From: Peggy Ruppel
Location: Biotech-Chem Library
REMSSEN 1B65
Phone: 571-272-2557

Peggy.Ruppel@uspto.gov

Search Notes

The results of your sequence search request are attached. Please contact me if you have any questions or comments.

Thank you for using STIC services.

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STIC-Biotech/ChemLib

138939

my

From: Gibbs, Terra
Sent: Tuesday, November 30, 2004 10:11 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search request...

Could you please do a regular search of SEQ ID NO:1 of USSN 09/491063 in all commercial and pending databases?
Could you please do a regular search of SEQ ID NO:2 of USSN 09/491063 in all commercial and pending databases?

Terra Cotta Gibbs, Ph.D.
Art Unit 1635
Remsen Building 2D10
Mailbox 2C18
571-272-0758

RECEIVED
NOV 30 2005
STIC/ChemLib Division
(STIC)

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

is Page Blank (uspto)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2004, 10:17:04 ; Search time 4769 Seconds
(without alignments)
10739.095 Million cell updates/sec

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Perfect score: 1083
Sequence: 1 atgcccccccaagaatt.....gcaatcagaagcgcgaggt 1083

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_ba:*
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3: gb_in:*
4: gb_om:*
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9: gb_pr:*
10: gb_ro:*
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12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	1076	99.4	2601	14 TMWALR	L14460 Tomato motc
2	1047.8	96.7	1086	14 TMWREPPRO	M90495 Tomato motc
3	1047.8	96.7	1162	6 AR170763	AR170763 Sequence
4	1044.6	96.5	1169	6 AR170765	AR170765 Sequence
5	1043	96.3	1169	6 AR170766	AR170766 Sequence
C 6	1040.8	96.1	2602	6 AR170774	AR170774 Sequence
7	1039.8	96.0	1169	6 AR170764	AR170764 Sequence
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C 10	856.4	79.1	2632	14 GEABMVA	X15983 Abutilon mo
C 11	840.4	77.6	2634	14 AMU51137	AMU51137 Abutilon mo
C 12	825.4	76.2	2634	14 AF101476	AF101476 Chino del
C 13	825	76.2	2155	14 TM056319	TM056319 Tomato mo
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C 16	814.2	74.8	2635	14 AF226665	AF226665 Chino del
C 17	809.8	74.4	2612	14 SGWV2612	Y11099 Sida yellow
C 18	806	74.4	2190	14 TLR488768	AJ488768 Tobacco 1
C 19	773.2	71.4	2615	14 BDMARAL13A	M88179 Bean dwarf

C 20	771.4	71.2	2603	14 SGWV2603	Y11097 Sida golden
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C 25	757.6	70.0	2620	14 HTVDANCA	Y14874 Tomato mosa
C 26	710.6	65.6	2584	14 TICY15034	Y15034 Potato yell
C 27	704.8	65.1	2593	14 PYVVA	D00940 Potato yell
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C 29	702.2	64.8	2644	14 AR170772	AR170772 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS Tomato mottle virus-[Florida] complete A component DNA; coat
DEFINITION protein (ARI), replicative protein (AL1), transcriptional element
(AL2), and AL3 genes, complete cds.

ACCESSION L14460
VERSION L14460.1 GI:295320
KEYWORDS Tomato mottle virus-[Florida]
SOURCE Tomato mottle virus-[Florida]
ORGANISM Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE 1 (bases 1 to 2601)
AUTHORS Abouzid,A.M., Poleton,J.E. and Hiebert,E.
TITLE The nucleotide sequence of tomato mottle virus, a new geminivirus
isolated from tomatoes in Florida
JOURNAL J. Gen. Virol. 73 (Pt 12), 3225-3229 (1992)
MEDLINE 93107858
PubMed 1469361

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ORIGIN

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Query Match      96.7%; Score 1047.8; DB 14; Length 1086;
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Matches 1061; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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DB 61 TGGCTCTTGTCTAAGAAAGACATTTCCCAATTAACAAACCTAAATACCCAGTCAAT 120

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RESULT 3
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DEFINITION Sequence 1 from patent US 6291743.
ACCESSION AR170763
VERSION AR170763.1 GI:17908722
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1162)
AUTHORS Stout,J.T., Liu,H.T., Hanson,S.F., Maxwell,D.P., Ahlquist,P.G. and
Gilbertson,R.L.
TITLE Transgenic plants expressing mutant geminivirus AC1 or CI genes
JOURNAL Patent: US 6291743-A 1 18-SEP-2001;
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Best Local Similarity 98.0%; Pred. No. 8.8e-293;
Matches 1061; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 ATGCCCCCACAAGAAATTAGAGTTCAGTCAAGAAAGACTATTTCTTAATTCCTCCAG 60
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QY 61 TGGCTCTATCTAAGAAAGACATTTCCCAATTAACAAACCTAAATACCCAGTCAAC 120
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QY 181 CTTGTTCAGTTCGAAGGTAAAGTACCAATGACGAATTAAGATTTCTTGAACCTGCTCC 240
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DEFINITION Sequence 5 from patent us 6291743.
ACCESSION AR10765
VERSION AR10765.1 GI:17908724
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1169)
AUTHORS Stout,J.T., Luu,H.T., Hanson,S.F., Maxwell,D.P., Ahlquist,P.G. and
TITLE Transgenic plants expressing mutant geminivirus AC1 or CI genes
JOURNAL Patent: US 6291743-A 5 18-SEP-2001;
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Db	1004	GCAGAAAATACAGGTCTTAAGAACTGGAATGCAATGCAAGATCGATCTTCATCACCTTCACA	1063
QY	1021	GCCTCCCTCTATCAAGAGACACACAGGCAAGCCAGAAACGGGCAATTCAGAAAGCGCAG	1080
Db	1064	GCCTCCCTCTATCAAGAGACACACAGGCAAGCCAGAAACGGGCAATTCAGAAAGCGCAG	1123
QY	1081	GGT 1083	
Db	1124	GGT 1126	

RESULT 6				
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ACCESSION	ARI170774			
VERSION	ARI170774.1	GI:17908733		
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 2602)			
	Scout,J.T., Luu,H.T., Hanson,S.F., Maxwell,D.P., Ahlquist,P.G. and			
	Gilbertson,R.L.			
TITLE	Transgenic plants expressing mutant geminivirus AC1 or CI genes			
JOURNAL	Patent: US 6291743-A 17 18-SEP-2001;			
FEATURES	Location/Qualifiers			
source	1..2602			
	/organism="unknown"			
	/mol_type="unassigned DNA".			
ORIGIN				
Query Match	96.1%;	Score 1040.8;	DB 6;	Length 2602;
Best Local Similarity	98.0%;	Pred. No. 1e-290;		
Matches 1054;	Conservative	0;	Mismatches 22;	Indels 0;
			Gaps	0;
Oy	8	CACCAAGAATTAGAGTTCAGTCAAGAAGACTATTTCCTAATCTATCCCAAGTGCCTC	67	
Db	2602	CACCAAGAATTAGAGTTCAGTCAAGAAGACTATTTCCTAATCTAATCCCAAGTGCCTT	2543	
Oy	68	TATCTAAAGAAGACCTTCCCAATTACAAAACTTAATACCCAGTCACACAGAAT	127	

Db 2542 TGTCTAAGAGAGACACTTCCCAATTACAAAACCTAATAATCCCAAGTCAATAAGAAAT 2483

Qy 128 TCATCAAAATTTGACAGAGAGCTTCATGAAAATGGGAAACCTCATCTCCATGCTGTTGTC 187

Db 2482 TCATCAAAATTTGACAGAGAGCTTCATGAAAATGGGAAACCTCATCTCCATGCTGTTGTC 2423

Qy 188 AGTTCGAAGGTAGTACCAATGACAGAAATACAGATTCTTGACCTGGTCTCCCAACCC 247

Db 2422 AGTTCGAAGGAAGTACCAATGACAGAAATACAGATTCTTGACCTGGTCTCCCAACCC 2363

Qy 248 GGTGACGACATTTCCATCCGAATATTCAGGGAGCTAAATCGAGCTCCGACGCTCAATCAT 307

Db 2362 GGTGACGACATTTCCATCCGAATATTCAGGGAGCTAAATCGAGCTCCGACGCTCAATCAT 2303

Qy 308 ACATCGACGAAGGAGGAGATACATCCGAATGGGAGATTTCCAAATCGACGGCAGATCTG 367

Db 2302 ACATCGACGAAGGAGGAGATACATCCGAATGGGAGATTTCCAAATCGACGGCAGATCTG 2243

Qy 368 CCAAGGAGGCGCAGAGCTCTGCTAATGATATATGCAAAAGCATTTAAATGACAGTTCCG 427

Db 2242 CCAAGGAGGCGCAGAGCTCTGCTAATGATATATGCAAAAGCATTTAAATGACAGTTCCG 2183

Qy 428 TTCAATCTGCTTAAAGGCTTAAAGGAAACAACCAAAAGATTTGTATTAACAAATC 487

Db 2182 TTCAATCTGCTTAAAGGCTTAAAGGAAACAACCAAAAGATTTGTATTAACAAATC 2123

Qy 488 ATTAACATCCGCTTAACCTTAAGCAATTCGCAAAAGCTCCGGAACCGTGGTCTC 547

Db 2122 ATTAACATCCGCTTAACCTTAAGCAATTCGCAAAAGCTCCGGAACCGTGGTCTC 2063

Qy 548 CATTTCAAGTCTCTTCTTCACTAAAGTTCCTGACGAGATCGAGAAATGGCGGATTAAT 607

Db 2062 CATTTCAAGTCTCTTCTTCACTAAAGTTCCTGACGAGATCGAGAAATGGCGGATTAAT 2003

Qy 608 ATTTGGGAGCGGAGCGCTCGCGCGCGGATTAAGCCTGTAAGTATCTGTCAGAGGTG 667

Db 2002 ATTTGGGAGCGGAGCGCTCGCGCGCGGATTAAGCCTGTAAGTATCTGTCAGAGGTG 1943

Qy 668 ATTTGAAGACGAGGAAGCAATGGGCGGTGATTAAGGCGCATTAATCATATCTCATG 727

Db 1942 ATTTGAAGACGAGGAAGCAATGGGCGGTGATTAAGGCGCATTAATCATATCTCATG 1883

Qy 728 GACACCTAGACCTTCAATGCTGAGTCTTCTGAAATGATGTCAGATTAACCTCATTTGATG 787

Db 1882 GACACCTAGACCTTCAATGCTGAGTCTTCTGAAATGATGTCAGATTAACCTCATTTGATG 1823

Qy 788 ACATCGCACCGCATTAATTAAGCTTAAGCACTGGAAGAAATGCTGGGGCCCAAGAA 847

Db 1822 ACATCGCACCGCATTAATTAAGCTTAAGCACTGGAAGAAATGCTGGGGCCCAAGAA 1763

Qy 848 ATTTGCAATCAAAATTTGACAGTAAAGCAAGTTCAAATTAAGGGGGAATCCAGCA 907

Db 1762 ATTTGCAATCAAAATTTGACAGTAAAGCAAGTTCAAATTAAGGGGGAATCCAGCA 1703

Qy 908 TCGTGTCTTTCGAATCTGCTGAGGGTGCACGCTAATAAGATTTTGAACAAGCAGAAA 967

Db 1702 TCGTGTCTTTCGAATCTGCTGAGGGTGCACGCTAATAAGATTTTGAACAAGCAGAAA 1643

Qy 968 ATACAGGCTCTAAGAACTGAGCTATCAAGAAATGGGATTTTATCACTCAGACCCGCC 1027

Db 1642 ATACAGGCTCTAAGAACTGAGCTATCAAGAAATGGGATTTTATCACTCAGACCCGCC 1583

Qy 1028 TCTATCAAGAGACGACAGGCAAGCCAAAGAAAGGGCAATCAGAAAGCGCGAGGT 1083

Db 1582 TCTATCAAGAGACGACAGGCAAGCCAAAGAAAGGGCAATCAGAAAGCGCGAGGT 1527

RESULT 7
ARI10764 1169 bp DNA linear PAT 17-DEC-2001
LOCUS ARI10764
DEFINITION Sequence 3 from patent US 6291743.
ACCESSION ARI10764
VERSION ARI10764.1 GI:17908723

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1169)
AUTHORS Scout, J. T., Luu, H. T., Hanson, S. F., Maxwell, D. P., Ahlquist, P. G. and Glibertson, R. L.
TITLE Transgenic plants expressing mutant geminivirus AC1 or CI genes
JOURNAL Patent: US 6291743-A 3 18-SEP-2001;
FEATURES Location/Qualifiers
1..1169
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 96.0%; Score 1039.8; DB 6; Length 1169;
Best Local Similarly 97.5%; Pred. No. 1.3e-290;
Matches 1056; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 1 ATGCCCCACCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTTAATCCAG 60

Db 44 ATGCCCCACCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTTAATCCAG 103

Qy 61 TGTCTCTATCTAAGAAAGAGACCTTCCCAATTACAAAACCTAATACCCAGTCAC 120

Db 104 TGTCTCTTGTCTAAGAAAGAGACCTTCCCAATTACAAAACCTAATACCCAGTCAT 163

Qy 121 AAGAAATTCATAAATTTGACAGAGCTTCATGAATAATGGGAACTCATCTCATGTG 180

Db 164 AAGAAATTCATAAATTTGACAGAGCTTCATGAATAATGGGAACTCATCTCATGTG 223

Qy 181 CTGTGAGTTCGAAGTAAAGTACCAATGACGAAATTAAGATTTCTGACCTGCTCC 240

Db 224 CTGTGAGTTCGAAGTAAAGTACCAATGACGAAATTAAGATTTCTGACCTGCTCC 283

Qy 241 CCAACCCGATCAGACATTTTCATCCGAATATTCAGGAGCTAATTCGAGCTCGAGTC 300

Db 284 CCAACCCGATCAGACATTTTCATCCGAATATTCAGGAGCTAATTCGAGCTCGAGTC 343

Qy 301 AATCATATCATCCAGACGAGAGATTAATGATGGGGAATTTCCAAATCGACGC 360

Db 344 AATCATATCATCCAGACGAGAGATTAATGATGGGGAATTTCCAAATCGACGC 403

Qy 361 AGATCTGCAAGAGGCGCAGAGTCTGCTAATGATTCATATGCGAAAGCATTAATGCA 420

Db 404 AGATCTGCAAGAGGCGCAGAGTCTGCTAATGATTCATATGCGAAAGCATTAATGCA 463

Qy 421 GGTTCGGTCAATCTGCTTAAAGCGGTTCTAAGGGAAGAACCAACCAAAATTTGATTA 480

Db 464 AGTTCGGTCAATCTGCTTAAAGCGGTTCTAAGGGAAGAACCAACCAAAATTTGATTA 523

Qy 481 CAAATATATAATCCGCTCTTAACCTTAGAAGCAATATTCGCAAAAGCTCCGGAACCGTGG 540

Db 524 CAAATATATAATCCGCTCTTAACCTTAGAAGCAATATTCGCAAAAGCTCCGGAACCGTGG 583

Qy 541 GTTCCTCATTTCAAGTCTCTTCTTCACTAAGTTCCTGACGAGATGACGAATGGGCG 600

Db 584 GTTCCTCATTTCAAGTCTCTTCTTCACTAAGTTCCTGACGAGATGACGAATGGGCG 643

Qy 601 GATTAATTAATTTGAGGAGCGGTTGACGCTGCGCGCGGATAGACCTGTAATCATCTGC 660

Db 644 GATTAATTAATTTGAGGAGCGGTTGACGCTGCGCGCGGATAGACCTGTAATCATCTGC 703

Qy 661 GAGGTGATTCAGAAACAGGGAAGACGATGGGCGGTGCTTAAAGCCCACTAATAT 720

Db 704 GAGGTGATTCAGAAACAGGGAAGACGATGGGCGGTGCTTAAAGCCCACTAATAT 763

Qy 721 CTCAGTGAACCTTGAAGTTCATGTCAGAGTCTTCTGCAATGATGTCAGTAAAGTC 780

Db 764 CTCAGTGAACCTTGAAGTTCATGTCAGAGTCTTCTGCAATGATGTCAGTAAAGTC 823

Qy 781 ATTGATGACATCGACCGCATTAATCTAAGCTAAGCACTGGAAGATTTGCTGGGGCC 840

Db 824 ATTAATAATACATGCGACCGCTTATCTAAAGCTTAAAGCATCTGGAAGAAATTGCTAGGGCC 883
QY 841 CAGAAAATTGGCAATCAATTGCAAGTACGCTAGCGCAAGTTCAAAATTAAAGCGGAATC 900
Db 884 CAGAAAGATTGGCAATCAATTGCAAGTACGCTAGCGCAAGTTCAAAATTAAAGCGGAATC 943
QY 901 CCAGCAATGCTGCTTTGCAATCTCTGGTAGGGGTCCAGCTATTAAGAATCTTTAGACAA 960
Db 944 CCAGCAATGCTGCTTTGCAATCTCTGGTAGGGGTCCAGCTATTAAGAATCTTTAGACAA 1003
QY 961 GCAGAAATACAGGCTCTCAAGAACTGACATCAAGAAATGCGATCTTCAATCAACCTCA 1020
Db 1004 GCAGAAATACAGGCTCTCAAGAACTGACATCAAGAAATGCGATCTTCAATCAACCTCA 1063
QY 1021 GCGCCCTCTATCAGAGACACACAGCGCAAGCAAGAAACGGGCAATCAGAAAGCGCAG 1080
Db 1064 GCGCCCTCTATCAGAGACACACAGCGCAAGCAAGAAACGGGCAATCAGAAAGCGCAG 1123
QY 1081 GGT 1083
Db 1124 GGT 1126

RESULT 8

LOCUS AR170771 1166 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 13 from patent US 6291743.
ACCESSION AR170771
VERSION AR170771.1 GI:17908730
KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1166)

AUTHORS Stout,J.T., Luu,H.T., Hanson,S.F., Maxwell,D.P., Ahlquist,P.G. and

TITLE Transgenic plants expressing mutant geminivirus AC1 or CI genes

JOURNAL Patent: US 6291743-A 13 18-SEP-2001;

FEATURES 1. 1166
source /organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 95.5%; Score 1033.8; DB 6; Length 1166;
Best Local Similarity 97.6%; Pred. No. 1e-288;
Matches 1061; Conservative 0; Mismatches 22; Indels 4; Gaps 1;

QY 1 ATGCCCCCAAGAAATTTAGAGTTCAAGTCAAAAGACTATTCTTCTTATCCCGAG 60
Db 44 ATGCCCCCAAGAAATTTAGAGTTCAAGTCAAAAGACTATTCTTCTTATCCCGAG 103
QY 61 TGTCTCTATCTTAAAGAGAGCACTTCCCAATTCAAAACCTAAATCCCGAGTCAAC 120
Db 104 TGTCTCTTGTCTTAAAGAGAGCACTTCCCAATTCAAAACCTAAATCCCGAGTCAAC 163
QY 121 AAGAAATTCATCAAAATTTGCAAGAGCTTCATGAATAATGGGAGCTCATCTCCATGTG 180
Db 164 AAGAAATTCATCAAAATTTGCAAGAGCTTCATGAATAATGGGAGCTCATCTCCATGTG 223
QY 181 CTGTGTCACTTGAAGAGTACGATCAATGACAGAAATGAGATTTCTTCACTGGTCTCC 240
Db 224 CTGTGTCACTTGAAGAGTACGATCAATGAGAGTATTCCTTCTTCACTGGTCTCC 283
QY 241 CCNACCCTGACATTTCCATTCGATATTCAGGAGCTTAATCGAGCTCCGAGTC 300
Db 284 CCNACCCTGACATTTCCATTCGATATTCAGGAGCTTAATCGAGCTCCGAGTC 343
QY 301 AATCATCATGACAGAGCGAGATATCAATGAAATGGGAGATTTCCAAATGACGCG 360
Db 344 AATCATCATGACAGAGCGAGATATCAATGAAATGGGAGATTTCCAAATGACGCG 403
QY 361 A----GATCTGCCAGAGAGCGCAGACGCTCTGTAATGATTCTATATGCGAAAGCATTA 416

Db 404 AGATCATCTGCGAGAGGCGCAGACGCTCTGTAATGATTCTATATGCGAAAGCGTTAA 463
QY 417 TGCAGGTTGCGTTCAATCTGCTTAGCGGTTCTAAGGAGAAACAACAAAGATTGT 476
Db 464 TGCAGGTTGCGTTCAATCTGCTTAGCGGTTCTAAGGAGAAACAACAAAGATTGT 523
QY 477 ATTACAAATCATTAATCTGCTTAACTGATAGACGAATATTTGCAAGGCTCCGAACC 536
Db 524 ATTACAAATCATTAATCTGCTTAACTGATAGACGAATATTTGCAAGGCTCCGAACC 583
QY 537 GTGGGTTCTCCATTTCAAGTCTCTTCTTCACTAAGTCTTCAAGAGATGAGGAATG 596
Db 584 GTGGGTTCTCCATTTCAAGTCTCTTCTTCACTAAGTCTTCAAGAGATGAGGAATG 643
QY 597 GGGGATTAATTAATTTGGAGCGGATGACCTGCGCGCGGATAGACTGTAATGATCAT 656
Db 644 GGGGATTAATTAATTTGGAGCGGATGACCTGCGCGCGGATAGACTGTAATGATCAT 703
QY 657 CGTGAAGGTGATTCAGAAACAGGGAAGACGATGTGGGCGGCTTGAAGCCCATTA 716
Db 704 CGTGAAGGTGATTCAGAAACAGGGAAGACGATGTGGGCGGCTTGAAGCCCATTA 763
QY 717 CTATCTCACTGACACCTGACTGCTCAATGTGAGTCTTCTGAAATGATGACATTA 776
Db 764 CTATCTCACTGACACCTGACTGCTCAATGTGAGTCTTCTGAAATGATGACATTA 823
QY 777 CGTCAATGATGACATGCAACCGCATTTATTAAGCTGAAGAAAGAAATTTGCTGAG 836
Db 824 CGTCAATGATGACATGCAACCGCATTTATTAAGCTGAAGAAAGAAATTTGCTGAG 883
QY 837 GGGCCAGAAAGATTGGCAATCAAAATTGCAAGTACGTAACCGATCAAAATTAAGCGG 896
Db 884 GGGCCAGAAAGATTGGCAATCAAAATTGCAAGTACGTAACCGATCAAAATTAAGCGG 943
QY 897 AATCCAGCAATCTGCTTGAATCTGCTGAGTGGAGGCTGACGCTTAAGAGTTCTTA 956
Db 944 AATCCAGCAATCTGCTTGAATCTGCTGAGTGGAGGCTGACGCTTAAGAGTTCTTA 1003
QY 957 CAAGAGCAAAATATACAGTCTCAAGATGAGTCAATCAAGAAATGCGATCTTCAACCT 1016
Db 1004 CAAGAGCAAAATATACAGTCTCAAGATGAGTCAATCAAGAAATGCGATCTTCAACCT 1063
QY 1017 CACAGCCCCCTCTATCAAGAGAGCACAGGCAAGCCAAAGAAACGGGCAATCAGAA 1076
Db 1064 CACAGCCCCCTCTATCAAGAGAGCACAGGCAAGCCAAAGAAACGGGCAATCAGAA 1123
QY 1077 GCAAGGT 1083
Db 1124 GCAAGGT 1130

RESULT 9

AF049336/c 2642 bp DNA linear VRL 06-MAR-1998

LOCUS AF049336 Sida golden mosaic virus coat protein (AV1), AC3 (AC3),

DEFINITION transactivator protein (AC2), replication associated protein (AC1),

and AC4 (AC4) genes, complete cds.

ACCESSION AF049336 GI:2935539

VERSION AF049336.1

KEYWORDS Sida golden mosaic virus

SOURCE Sida golden mosaic virus

ORGANISM Viruses; ssDNA viruses; Geminiviridae; Begomovirus.

REFERENCE 1 (bases 1 to 2642)
AUTHORS Abouzid,A.M., Polston,J.E. and Hiebert,E.
TITLE Molecular characterization of a geminivirus infecting Sida
santaremensis in Florida
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2642)
AUTHORS Abouzid,A.M., Polston,J.E. and Hiebert,E.
TITLE Direct Submission
JOURNAL Submitted (19-FEB-1998) Plant Pathology, University of Florida,

1435 Fifield Hall, PO Box 110680, Gainesville, FL 32611-0680, USA

FEATURES
Location/Qualifiers

1. .2642

/organism="Sida golden mosaic virus"

/mol_type="genomic DNA"

/isolate="Florida"

/db_xref="taxon:51034"

1. .178

359. .1114

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/gene="AV1"

/codon_start=1

/product="coat protein"

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/db_xref="GI:2935540"

/translation="MPKRELPMRSMAGTSKYSHNANSPRAGSGPRVHKASWVNRBM
YKRAIRYMRVTPDVPKCEGCEPKVQSEORHDI SHGKVMCISDVTGNGITHRVGK
RPECVSYIIGKIMDENIKLKHNTSVMFLVDRDRPGTGMDFGVFMDFNEPST
ATYKNDLRDRYVMHMKRYKVTGGVANSNOAIVKRWKNHNVVNHQAGKYENHT
ENALLVMACTHASNPHYATLKIRITYDSLAM"

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complement (1111. .1509)

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/db_xref="GI:2935543"

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YHVIQRENHMLRRLALHLKALFNFOVTTSTMTASGYLARFLVLMYDQIGIISL
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complement (1256. .1645)

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complement (1256. .1645)

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genes"

/codon_start=1

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/protein_id="AAC05153.1"

/db_xref="GI:2935542"

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GHGTIRGHICTSGEMRYLIGRKSPLFDIQCRPALHQHNDI PRTDKVPQPE
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complement (1557. .2642)

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ONNIRSENLERIFAKABEPWPVPROLSINVDDEMOMADEPFGSSAARPLST
IVGDSRTGKTMARALAGPHNYLSGHLDPNGRYSNENNVNIDVAPQYLKAKHKE
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APPSLSLTSTTVYQWNGESSRSTADQLEASRLIMHQR"Best Local Similarity 89.9%; Pred. No. 1,9e-251;
Matches 971; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

Qy	1	ATGCCCCCAAGAAATTTAGAGTTCAAGAACTATTTCTTAATCTTACCCAG	60
Db	2642	ATGCCACCGCAAGAAATTTAGAGTTCAAGAACTATTTCTTATCCACAG	2583
Qy	61	TGCTCTCTATCTAAAGAAAGACCTTCCCAATTAACAAACCTTAATACCCAGTCAAC	120
Db	2582	TGCTCTGACCAAGAAAGACCTTCCCAATTAACAAACCTTAATACCAAGTCAAC	2523
Qy	121	AGAATTCATCAAAATTTGACAGAGCTTCATGAAATGAGGAACTCATCTCATGTG	180
Db	2522	AGAAGTTTCATCAAAATTCGACAGAGCTTCAGAAATGAGGAGCTCATCTCATGTG	2463
Qy	181	CTTGTCAGTTGCAAGTAAGTACCAATGACCAATACCAATTCATTCCTGCTCC	240
Db	2462	CTCTACAGTTGCAAGGAAATACCAATGACCAATACCAATTCATTCCTGCTCC	2403
Qy	241	CCAAACCGGTCAGACATTTCCATCCGAATATTCAGGAGCTAAATGAGCTCGACGTC	300
Db	2402	CCAAACGTCAGACATTTCCATCCGAATATTCAGGAGCTAAATGAGCTCGACGTC	2343
Qy	301	AAATCATATCATCGACCAAGACGAGATACCAATGAGGAGATTTCCAAATCGACGC	360
Db	2342	AAATCATATCATCGACCAAGACGAGATACCAATGAGGAGATTTCCAAATCGACGC	2283
Qy	361	AGATCTGCCAGAGAGGCCGACGCTGCTTAATGATTCATATGCGAAAGCATTAATGCA	420
Db	2282	AGATCTGCCAGAGAGGCCGACGCTGCTTAATGATTCATATGCGAAAGCATTAATGCA	2223
Qy	421	GGTTGGGTCATCTGCTTACGGGCTTCTAAGGAAAGAAACCAACCAAAAGATTTGTATTA	480
Db	2222	GATTCGTTCAATCTGCTTACGGGCTTCTAAGGAAAGAAACCAACCAAAAGATTTGTATTA	2163
Qy	481	CAAAATCATTAATCCGCTCTTAACCTTAAGAAAGATTTGCAAAAGCTCCGAAACGCTGG	540
Db	2162	CAGATCATTAATCCGCTCTTAAGAAAGATTTGCAAAAGCTCCGAAACGCTGG	2103
Qy	541	GTTCTTCATTTCAAGTCTTCTTTCACTAAGTTCCTTAAGAGATGACAGAAATGGGCG	600
Db	2102	GTTCTTCATTTCAAGTCTTCTTTCACTAAGTTCCTTAAGAGATGACAGAAATGGGCG	2043
Qy	601	GATATATTTTGGGAGGGGTGACGCTGCGCGCGGATGACCTGTAATATCATCTGTC	660
Db	2042	GATGAATTTTGGTTCGCTTCGCTGCGCGCGGATGACCTGTAATATCATCTGTA	1983
Qy	661	GAGGATATTCAGAAACAGGAAAGACGATGAGGCGGCTGTTAGGCCCAATATCTAT	720
Db	1982	GAGGATATTCAGAAACAGGAAAGACGATGAGGCGGCTGTTAGGCCCAATATCTAT	1923
Qy	721	CTAGTGAACAACCTAAGCTTCAATGTGTCAGTCTTCTCGAATGATGACGATTAACGTC	780
Db	1922	CTAGTGAACAACCTAAGCTTCAATGTGTCAGTCTTCTCGAATGATGACGATTAACGTC	1863
Qy	781	ATTGATGATTCGACGCGCATTTCTTAAGCTTAAGCACTGGAAGAATGCTGGGGCC	840
Db	1862	ATTGATGATTCGACGCGCATTTCTTAAGCTTAAGCACTGGAAGAATGCTGGGGCC	1883
Qy	841	CAGAAAGATTGGCAATCAAAATTCGAATGCGTAAGCAGTTCGAATTAAGCGGATC	900
Db	1802	CAAAAAGATTGGCAATCAAAATTCGAATGCGTAAGCAGTTCGAATTAAGCGGATC	1743
Qy	901	CCAGCAATCGTCTTTGCAATCTGTCGAGAGGTCGACGTAATAAGGCTCTTAGACAA	960
Db	1742	CCAGCAATCGTCTTTGCAATCTGTCGAGAGGTCGACGTAATAAGGCTCTTAGACAA	1683
Qy	961	GCAGAAATATCAGATCTCAAGAACTGATCAATCAAGATCGATCTTCATCACCTTACA	1020
Db	1682	GAGAAATATCAGATCTCAAGAACTGATCAATCAAGATCGATCTTCATCACCTTACA	1623
Qy	1021	GCCCCCTTATCAAGAGACACAGGCAAGCCAAAGAAACGCGCAATCAAGAGCGCAG	1080

ORIGIN

Query Match

83.6%; Score 905.6; DB 14; Length 2642;

Db 1622 GCCCCTCTATACAGACACACAGCGCCAGAGAGGCGCATACGAGCGGAG 1563

RESULT 10
LOCUS GEABMV/c 2632 bp DNA circular VRL 21-NOV-2003
DEFINITION Abutillon mosaic virus subgenome DNA A.
ACCESSION X15983
VERSION X15983.2 GI:38490457
KEYWORDS circular; coat protein; structural protein.
SOURCE Abutillon mosaic virus
ORGANISM Abutillon mosaic virus
vireuses; sedna vireuses; Geminiviridae; Begomovirus.

REFERENCE 1 (bases 1 to 2632)
AUTHORS Frieschmidt, T., Zimmert, G. and Jeske, H.
TITLE The nucleotide sequence of abutillon mosaic virus reveals virology 178 (2), 461-468 (1990)

JOURNAL MEDLINE 91020984
PUBMED 2219703
REFERENCE 2 (bases 1 to 2632)
AUTHORS Jeske, H.
TITLE Direct Submission
JOURNAL Submitted (26-JUL-1989) Jeske H., Institut f Allgemeine Botanik, Universitaet Hamburg, Ohnhorst str 18, 2000 Hamburg 52, F R G
REMARK revised by [3]

REFERENCE 3
AUTHORS Jeske, H.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-1990)
REMARK revised by [4]
AUTHORS Jeske, H.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2003) Jeske H., Biologisches Institut, Pfaffenwaldring 57, D-70550 Stuttgart, GERMANY
COMMENT On Nov 21, 2003 this sequence version replaced gi:59349.
FEATURES
source
1. .2632
/organism="Abutillon mosaic virus"
/mol_type="genomic DNA"
/specific_host="Abutillon bellioianum REGEL"
/db_xref="taxon:10815"
/segment="DNA A"
complement(join(1571..2632,1..9))
/gene="ORF C1"
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/db_xref="GI:38490459"
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/translation="MPPEKKFRYQAKYVPLTTPQCSLTDEALSQLQNLTPYKRFI
KICRELHENGEPHLVLIQPEKTYQCTNNFPLVPSPTSAHPNVIQAKSSDVKS
YIDKDDTIAEWGEFOIDGRSARGQQTANDSVAKALNAGVQALNLIKESQKDYVL
QNNINISNLERIIPAKAPEPVPFRPLSPFAVPEQWADYFGSGSAPRPPSL
IYVGDRTGKTWAKALGPHNYLSGLIDFGRVYSNVEYNVDVAAPHYLRKHKWE
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IPTTLTAPLYQESTONGQBEHG"
358..1113
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/db_xref="SwIs8-Prot:P21942"
/translation="MPKRDLPMSMGPTSTSRNANVSPRARIQPRVDKASEWVHRPM
YRKRPIYRTLTADVPKRGCGKQSYEGRHDI SHGKVMCI SDVTRNGNITHRGK

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388..1110
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complement(1110..1508)
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/db_xref="GI:59352"
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VERSION AF101476.1 GI:4336693
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SOURCE Chino del tomate virus-[IC]
ORGANISM Viruses; sedna viruses; Geminiviridae; Begomovirus.
REFERENCE 1 (bases 1 to 2634)
AUTHORS Jiang, H., Hou, Y.-M., Guzman, P. and Gilbertson, R.L.
TITLE Complete nucleotide sequence of the infectious clone of tomato leaf crumple geminivirus
JOURNAL (in) ANNUAL MEETING OF THE AMERICAN PHYTOPATHOLOGICAL SOCIETY, PHYTOPATHOLOGY, VOL 88 (SUPPL): S44; (1998)
2 (bases 1 to 2634)
REFERENCE Jiang, H., Hou, Y.-M., Guzman, P. and Gilbertson, R.L.
AUTHORS Submitted (26-OCT-1998) Plant Pathology, University of California, Davis, One Shields Ave., Davis, CA 95616, USA
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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12	694.6	64.1	1183	2 AAT93290	Aat93290 Bean gold
13	694.6	64.1	1651	3 AAA94701	Aaa94701 pTrep23 nu
14	691.2	63.8	1062	2 AAT93291	Aat93291 Bean gold
15	691.2	63.8	1062	2 AAT93292	Aat93292 Bean gold
16	689.6	63.7	1062	2 AAT93293	Aat93293 Bean gold
17	683.8	63.1	2647	1 AAN60611	Aan60611 Vector se
18	683.8	63.1	2647	1 AAN70630	Aan70630 DNA -b se
19	496	45.8	1695	2 AAQ84378	Aa84378 Tomato ye
20	494.4	45.7	1080	2 AAT12905	Aat12905 Sardinian
21	492.8	45.5	1080	2 AAT12905	Aat12905 Sardinian

22	492.8	45.5	1080	2 AAT12904	Aat12904 Sardinian
23	479.4	44.3	1145	2 AAT93287	Aat93287 Tomato ye
24	479.4	44.3	1145	2 AAT93288	Aat93288 Tomato ye
25	479.4	44.3	1145	2 AAT93311	Aat93311 Tomato ye
26	476.2	44.0	1145	2 AAT93289	Aat93289 Tomato ye
27	474	43.8	2739	2 AAT21646	Aa21646 Tomato le
28	448	41.4	2766	2 AAV29761	Aav29761 Tobacco l
29	421.2	38.9	2723	1 AAN70893	Aan70893 MYRV extra
30	419.6	38.7	1083	1 AAN70897	Aan70897 ORF 4 firo
31	418.4	38.6	2744	2 AAT93317	Aat93317 Tomato le
32	304.4	28.1	691	8 ABV76265	Abv76265 Tomato ye
33	259.4	24.0	506	8 ABV76265	Abv76265 Tomato ye
34	259.4	24.0	506	8 ABV76263	Abv76263 Tomato ye
35	259.4	24.0	508	8 ABV76264	Abv76264 Tomato ye
36	251	23.2	550	2 AAQ84375	Aa84375 Tomato le
37	246.6	22.8	1403	2 AAT93318	Aat93318 Tomato-in
38	243.8	22.5	550	2 AAQ84377	Aa84377 Tomato le
39	238.2	22.0	550	2 AAQ84376	Aa84376 Tomato le
40	185.2	17.1	780	2 AAT93319	Aat93319 Tomato-in
41	183.8	17.0	479	2 AAQ84372	Aa84372 Gemini vi
42	162	15.0	297	1 AAN70900	Aan70900 ORF 7 firo
43	158	14.6	434	2 AAQ84371	Aa84371 Gemini vi
44	80.2	7.4	270	2 AAQ84370	Aa84370 Gemini vi
45	50.2	4.6	795	3 AAZ49876	Aaz49876 Wheat dwa

ALIGNMENTS

RESULT 1	
AAT93294	
ID AAT93294 standard; DNA; 1160 BP.	
XX	
AC AAT93294;	
XX	
DT 17-OCT-2003 (revised)	
DT 27-APR-1998 (first entry)	
XX	
DE Tomato mottle virus AC1 open reading frame.	
XX	
DE Tomato mottle virus AC1 open reading frame.	
XX	
KW Geminiivirus; TOMOV; AC1 gene; transdominant mutation; transgenic plant;	
KM disease resistance; ss; cyclic; circular.	
XX	
OS Tomato mottle virus; isolate Florida.	
XX	
FH Key	Location/Qualifiers
FT CDS	44..1129
FT	/*tag= a
XX	
PN WO9739110-AI.	
XX	
PD 23-OCT-1997.	
XX	
PE 15-APR-1997; 97MO-US006300.	
XX	
PR 16-APR-1996; 96US-0015517P.	
XX	
PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.	
PA (WISC) WISCONSIN ALUMNI RES FOUND.	
XX	
PI Scout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;	
XX	
XX WPI; 1997-526447/48.	
DR P-PSDB; AAW34332.	
XX	
PT Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant	
PT genes - have increased resistance to geminivirus infection e.g. tomato	
PT mottle virus, tomato yellow leaf curl virus or Bean golden mosaic	
PT geminivirus.	
XX	
PS Example 3.3; Page 57-58; 132bp; English.	
XX	
CC This genomic DNA sequence includes the open reading frame of the wild-	

CC type AC1 gene of tomato mottle virus (Tomov), a geminivirus that has a
 CC bipartite genome. The AC1 gene must be expressed for efficient
 CC replication of the two genomic components, DNA-A and DNA-B. It encodes a
 CC protein (see AAW34336) having a DNA binding site specific to the DNA-A
 CC common region, a DNA nicking activity, and an NTP binding activity. The
 CC invention involves production of transgenic plants containing DNA
 CC comprising AC1 or CI wild-type or mutant sequences that negatively
 CC interfere in trans with geminiviral replication during infection. Such
 CC transgenic plants are resistant to viral infection. The AC1/CI genes are
 CC especially from Tomov, tomato yellow leaf curl virus or bean golden
 CC mosaic geminivirus (see AAT93282-93) and encode polypeptides (see
 CC AAW34324-35) that have mutations in the highly conserved DNA-nicking
 CC domain and/or the NTP-binding domain. (Updated on 17-OCT-2003 to
 CC standardise OS field)

XX Sequence 1160 BP; 360 A; 276 C; 257 G; 267 T; 0 U; 0 Other;

Query Match 96.7%; Score 1047.8; DB 2; Length 1160;

Best Local Similarity 98.0%; Pred. No. 0;

Matches 1061; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 ATGCCCCCACCAGAAATTTAGAGTTCAAGTCAAAAGAACTATTTCTCACTTATCCCAAG 60
 DB 44 ATGCCCCCACCAGAAATTTAGAGTTCAAGTCAAAAGAACTATTTCTCACTTATCCCAAG 103
 QY 61 TGCTCTCTATCTAAGAGAGACCTTCCCAATTACAAAACCTAAATACCCCAAGTCAAC 120
 DB 104 TGCTCTCTATCTAAGAGAGACCTTCCCAATTACAAAACCTAAATACCCCAAGTCAAT 163
 QY 121 AAGAAATTCATCAAAATTTTGAGAGAGCTTCATGAAAATGGGAACTCTCATCTCATGTG 180
 DB 164 AAGAAATTCATCAAAATTTTGAGAGAGCTTCATGAAAATGGGAACTCTCATCTCATGTG 223
 QY 181 CTGTGTTCAAGTTCCAAAGTAAATGCAATGCAAGATTAACAGATTCTTCGACCTGTCTCC 240
 DB 224 CTGTGTTCAAGTTCCAAAGTAAATGCAATGCAAGATTAACAGATTCTTCGACCTGTCTCC 283
 QY 241 CCAACCCGGTCCAGACATTTTCATCCGAATTTTGAAGAGCTAAATGAGAGTCCGAGATC 300
 DB 284 CCAACCCGGTCCAGACATTTTCATCCGAATTTTGAAGAGCTAAATGAGAGTCCGAGATC 343
 QY 301 AAATCATACATCGACAAAGAGAGATACATCGAATGGGAGATTTCCAAATGACGCGC 360
 DB 344 AAATCGTACATCGACAAAGAGAGATACATCGAATGGGAGATTTCCAAATGACGCGC 403
 QY 361 AGATCTGCCAGAGAGAGCGCAGACATCTGCTAATGATTCATATGCGAAGCATTTAAATGCA 420
 DB 404 AGATCTGCCAGAGAGAGCGCAGACATCTGCTAATGATTCATATGCGAAGCATTTAAATGCA 463
 QY 421 GGTTGCGTTCAATCTGCTTACGCGTTCTAAGGGAAGAACCAAAAGATTTTGTATTA 480
 DB 464 AGTTGCGTTCAATCTGCTTACGCGTTCTAAGGGAAGAACCAAAAGATTTTGTATTA 523
 QY 481 CAAATATATACATCGCTCTTAACCTTAGAAGAAATTTCCGAAAGGCTCCGGAACCGGTG 540
 DB 524 CAAATATATACATCGCTCTTAACCTTAGAAGAAATTTCCGAAAGGCTCCGGAACCGGTG 583
 QY 541 GTTCTCTCATTTCAAGTCTCTTTCTTCACTAAGCTTTCTGACGAGATGCGAAGATGGGCG 600
 DB 584 GTTCTCTCATTTCAAGTCTCTTTCTTCACTAAGCTTTCTGACGAGATGCGAAGATGGGCG 643
 QY 601 GATATATATTTCCGAGCGGTGACGCTGCGCGCGGATAGACCTGTAAGTATCATGCTC 660
 DB 644 GATATATATTTCCGAGCGGTGACGCTGCGCGCGGATAGACCTGTAAGTATCATGCTC 703
 QY 661 GAGGGTATTTCAAGAACGAGGAACGATGTGGCGGTGGTGAAGGCCCAATTAATAT 720
 DB 704 GAGGGTATTTCAAGAACGAGGAACGATGTGGCGGTGAAGGCCCAATTAATAT 763
 QY 721 CTGAGTGAACCTTAAGCTTCAATGCTGAGTCTTTCTGCAATGATGTCAGTATTAAGCTC 780
 DB 764 CTGAGTGAACCTTAAGCTTCAATGCTGAGTCTTTCTGCAATGATGTCAGTATTAAGCTC 823

QY 781 ATGATGACATCGACCGCATTTATCTTAAGCTAAAGCAGTGAAGAAATTTGCTGGGCGC 840
 DB 824 ATGATGACATCGACCGCATTTATCTTAAGCTTAAGCAGTGAAGAAATTTGCTGGGCGC 883
 QY 841 CAGAAAGATTGGCAATCAATCAATTCAGTAAGCAGTGAAGCAGTTCATTAAGGCGGAATC 900
 DB 884 CAGAAAGATTGGCAATCAATCAATTCAGTAAGCAGTGAAGCAGTTCATTAAGGCGGAATC 943
 QY 901 CAGCAATCTGCTTTGCAATCTCTGTGAGAGGTCGCGCTTAAGAGTCTTAAGACAA 960
 DB 944 CAGCAATCTGCTTTGCAATCTCTGTGAGAGGTCGCGCTTAAGAGTCTTAAGACAA 1003
 QY 961 GCAGAAATACAGGTCTCAAGACTGAGTATCAAGATGCAATCTTCATCACCTCACA 1020
 DB 1004 GCAGAAATACAGGTCTCAAGACTGAGTATCAAGATGCAATCTTCATCACCTCACA 1063
 QY 1021 GCCCCTCTATCAAGAGACACACAGGCAAGCCAGAAACGGGCAATCGAAGCGCAG 1080
 DB 1064 GCCCCTCTATCAAGAGACACACAGGCAAGCCAGAAACGGGCAATCGAAGCGCAG 1123
 QY 1081 GGT 1083
 DB 1124 GGT 1126

RESULT 2

AAT93283 standard; DNA; 1169 BP.

AAT93283;

27-Apr-1998 (first entry)

Tomato mottle virus AC1 mutant Tomov-AC1d1m1 gene.

Geminivirus; Tomov-AC1d1m1; AC1 gene; transdominant mutation;

transgenic plant; disease resistance; ss; cyclic; circular.

Tomato mottle virus; isolate Florida.

Synthetic.

Key Location/Qualifiers

CDS 44..1129

FT /*tag= a

XX W09739110-A1.

XX 23-OCT-1997.

XX 15-APR-1997; 97MO-US006300.

XX 16-APR-1996; 96US-0015517P.

XX (SEMT-) SEMINIS VEGETABLE SEEDS INC.

XX (WISC) WISCONSIN ALUMNI RES FOUND.

XX Scout UT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;

XX WPI, 1997-526447/48.

XX P-PSDB; AAW34325.

XX Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant

PT genes - have increased resistance to geminivirus infection e.g. tomato

PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic

PT geminivirus.

XX Claim 11; Page 64-65; 132pp; English.

XX This DNA sequence comprises a transdominant lethal mutant, designated

CC Tomov-AC1d1m1, of the AC1 gene of tomato mottle virus (Tomov). It

CC encodes an AC1 protein (see AAW34325) that carries a mutation in its NTP-

CC binding domain. The AC1 gene (see also AAT93294) must be expressed for

CC efficient replication of the two genomic components, DNA-A and DNA-B, of

CC the bipartite ToMV genome. The invention involves production of
CC transgenic plants containing DNA comprising geminiviruses Ac1 or Ct wild-
CC type or mutant sequences that negatively interfere in trans with
CC geminiviral replication during infection. Such transgenic plants are
CC resistant to viral infection. The Ac1/Ct genes are especially from ToMV,
CC tomato yellow leaf curl virus or bean golden mosaic geminivirus (see
CC AM933282-93) and encode polypeptides (see AM93424-35) that have
CC mutations in the highly conserved DNA-nicking and/or the NTP-binding
CC domains

SQ Sequence 1169 BP; 361 A; 280 C; 258 G; 270 T; 0 U; 0 Other;

Query Match	96.5%	Score 1044.6;	DB 2;	Length 1169;
Best Local Similarity	97.9%	Prod No. 0		

Matches 1059; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY	1	ATGCCCCACCAAAATAATTGAGTTCAGTCAAAAGACTATTTTCTTAATCTTATCCCG	60
Db	44	ATGCCCCACCAAAATAATTGAGTTCAGTCAAAAGACTATTTTCTTAATCTTATCCCG	103
QY	61	TGCTCTATCTTAAAGAAAGCACTTTCCTTAATCAAAACCTTAATATCCCAAGTCAAC	120
Db	104	TGCTCTATCTTAAAGAAAGCACTTTCCTTAATCAAAACCTTAATATCCCAAGTCAAT	163
QY	121	AAGAAATTCATCAAAATTTGCGAGAGCTTCATGAAAAAGGGGAACCTCATCTCCATGCG	180
Db	164	AAGAAATTCATCAAAATTTGCGAGAGCTTCATGAAAAAGGGGAACCTCATCTCCATGCG	223
QY	181	CTTGTTCAAGTCGAAGGTAAAGTACCAATGCAAGAAATACAGATTTCTTCGACCTGGCTCC	240
Db	224	CTTGTTCAAGTCGAAGAAAGTAAAGTACCAAGTAAAGATTTCTTCGACCTGGCTCC	283
QY	241	CCAAACCCGGTCAGCACTATTTCCATCCGAATATTCAGGGAGCTAAATCGAGCTCCGAGTC	300
Db	284	CCAAACCCGGTCAGCACTATTTCCATCCGAATATTCAGGGAGCTAAATCGAGCTCCGAGTC	343
QY	301	AAATCATATCATCGAACAAAGACGGAATCAATCGAATGGGGAGATTTCCAAATTCGACGGC	360
Db	344	AAATCATATCATCGAACAAAGACGGAATCAATCGAATGGGGAGATTTCCAAATTCGACGGC	403
QY	361	AGATCTGCGCAGAGAGGCGCAGCAGTCTGCTAAATGAATTCATATGCGAAAGCATTAATGCA	420
Db	404	AGATCTGCGCAGAGAGGCGCAGCAGTCTGCTAAATGAATTCATATGCGAAAGCATTAATGCA	463
.QY	421	GGTTCGGTTCATCTGCTTACCGGTTCTAAAGGAAAGCAACCAAAAGATTTTGTATTA	480
Db	464	AGTTCGGTTCATCTGCTTACCGGTTCTAAAGGAAAGCAACCAAAAGATTTTGTATTA	523
QY	481	CAAAATCATTAACATCCGCTCTAACTTAAGAACAAATATTCGAAAGGCTCCGGAAACCGTGG	540
Db	524	CAAAATCATTAACATCCGCTCTAACTTAAGAACAAATATTCGAAAGGCTCCGGAAACCGTGG	583
QY	541	GTTCTCGATTTCAAGTCTCTTCTTCACTAACGTTCTTGACGAGATGCGAATGGGGCG	600
Db	584	GTTCTCGATTTCAAGTCTCTTCTTCACTAACGTTCTTGACGAGATGCGAATGGGGCG	643
QY	601	GATAATTAATTTCCGGAGCGGGTGAACCTCGGCGCCGGAGTAAGACCTGTAAATATCATCTGTC	660
Db	644	GATAATTAATTTCCGGAGCGGGTGAACCTCGGCGCCGGAGTAAGTAATATCATCTGTC	703
QY	661	GAGGGTGAATTCAGAAACAGAGGAAGACGATGTGGGGCGCTGCTTAAGCCACATTAATCTAT	720
Db	704	GAGGGTGAATTCAGAAACAGAGGAAGACGATGTGGGGCGCTGCTTAAGCCACATTAATCTAT	763
QY	721	CTCACTGGAACACTTGAATTTCAATGGTGAAGTCTTCTGAAATGATGTGCAATTAACGTC	780
Db	764	CTCACTGGAACACTTGAATTTCAATGGTGAAGTCTTCTGAAATGATGTGCAATTAACGTC	823
QY	781	ATTGATGACATGCGACCGCATTTATCTTAAAGCTTAAAGCACTGGAAGAAATTTGCTAAGGGGCC	840
Db	824	ATTGATGACATGCGACCGCATTTATCTTAAAGCTTAAAGCACTGGAAGAAATTTGCTAAGGGGCC	883
QY	841	CAGAAAGATTGGCAATCAAAATTCGAAGTACGGGTAAAGCCAGTTTCAAAATTAAGCGGGAATC	900

Db	884	CAGAAAGATTGGCAATCAAAATTGGCAATAGCGGTACAGATTCAAATTTAAAGGGCGAATC	943
QY	901	CCACCAATCGGCTTTGGCAATCCGTGGTGAAGGGGCCAGCTATATAAGATTCTTAGACAAA	960
Db	944	CCAGCAATTCGTCTTTGCCATCTCGTGAGGGGTCCAGCTATATAAGATTCTTAGACAAA	1003
QY	961	GCAGAAATACAGGCTTCAGAACTGAGCTATCAGAATGGCATCTTCATCACCTTCACA	1020
Db	1004	GCAGAAATACAGGCTTCAGAACTGAGCTATCAGAATGGCATCTTCATCACCTTCACA	1063
QY	1021	GCCTCCCTCTATCAAGAGACACACAGGCAGCCAGAAACCGGCAATCAGAAAGCGCAG	1080
Db	1064	GCCTCCCTCTATCAAGAGACACACAGGCAGCCAGAAACCGGCAATCAGAAAGCGCAG	1123
QY	1081	GCT 1083	
Db	1124	GCT 1126	

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RESULT 3
AAT93284
ID AAT93284 standard; DNA; 1169 BP.

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AC AAT93284;

DT 27-APR-1998 (first entry)

DE Tomato mottle virus AC1 mutant TOMOV-AC1d1m23 gene.

KW Geminivirus; TOMOV-AcIdIm23; AC1 gene; transdominant mutation;

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05 Synthetic.
xy

FH	Key	Location/Qualifiers
ET	CNC	44 1139

ET
yy

/*tag= a .

PN WO9739110-A1.

PD 23-OCT-1997.
YY

PF 15-APR-1997; 97WC-US0006300.
XX

PR 16-APR-1996; 96US-0015517P.
XX

PA (SEMI-) SEMINIS VEGETABLE SEEDS INC
(WISC) WISCONSIN ALLIUM PES EOUND
BA

XX
BT
Stout JT
Hanson SE
Maxwell J
DB
ahj
twist
BC:

XX WDT, 1997-536447/48
DP

DR P-PSDB; AA034326.
XX

PT Transgenic plants expressing geminivirus AcI and CI wild-type and mutant genes - have increased resistance to geminivirus infection and tomato

PT	mottle virus, tomato yellow leaf curl virus or bean golden mosaic
PT	geminivirus

XX
PS Claim 11: Page 67-69: 132nd: English

XX This DNA sequence comprises a transduc

tomov-AcIdim23, of the ACI gene of tomato mottle virus (tomov). CC encodes an ACI protein (see AAW34326) that carries 2 mutations in an

efficient replication of the two genomic components. DNA-A and DNA-B, 8 cc binding domain. The ACl gene (see also AAI93294) must be expressed for

transgenic plants containing DNA comprising geminivirus AC1 or CI wild-

CC type or mutant sequences that negatively interfere in trans with
CC geminiviral replication during infection. Such transgenic plants are

cc resistant to viral infection. The HCl/Cr genes are especially from 100%

CC tomato yellow leaf curl virus or bean golden mosaic geminivirus (see
 CC AAT93382-93) and encode polypeptides (see AAM3324-35) that have
 CC mutations in the highly conserved DNA-nicking and/or the NTP-binding
 CC domains
 CC XX

Sequence 1169 BP; 364 A; 278 C; 257 G; 270 T; 0 U; 0 Other;

Query Match 96.3%; Score 1043; DB 2; Length 1169;

Best Local Similarity 97.7%; Pred. No. 0; Mismatches 25; Indels 0; Gaps 0;

Matches 1058; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGCCCCCAGCAAGAAATTTAGAGTTCAATCAAGAACTATTTCTTACTTATCCCGAG 60
 DB 44 ATGCCCCCAGCAAGAAATTTAGAGTTCAATCAAGAACTATTTCTTACTTATCCCGAG 103
 QY 61 TGTCTCTATTAAGAAAGACACTTCCCAATTAACAAACCTAATACCCGAGTCAAC 120
 DB 104 TGTCTCTATTAAGAAAGACACTTCCCAATTAACAAACCTAATACCCGAGTCAAT 163
 QY 121 AAGAAATTCATCAAAATTTGAGAGAGGTTGATGAGAAATGGGGAACCTCATCTCATGTG 180
 DB 164 AAGAAATTCATCAAAATTTGAGAGAGGTTGATGAGAAATGGGGAACCTCATCTCATGTG 223
 QY 181 CTGTGTCAGTTCAGAGGTAGTACCAATGCAAGATTAACAGATTCTTGACCTGTCTCC 240
 DB 224 CTGTGTCAGTTCAGAGGTAGTACCAATGCAAGATTAACAGATTCTTGACCTGTCTCC 283
 QY 241 CCAACCCGGGTAGACATTTTCATCCCAATTTTACGGGAGCTTAATGAGCTCCGAGTCC 300
 DB 284 CCAACCCGGGTAGACATTTTCATCCCAATTTTACGGGAGCTTAATGAGCTCCGAGTCC 343
 QY 301 AATCATATCATGCAAGAGAGCGAGATPACATGCAATGCAATGGGAGATTTCCTAATGCAAGCGC 360
 DB 344 AATCATATCATGCAAGAGAGCGAGATPACATGCAATGCAATGGGAGATTTCCTAATGCAAGCGC 403
 QY 361 AGATCTGCGAGAGAGCGAGAGCTGTGCTAATGATTAATGCGAAAGCTTAATGCA 420
 DB 404 AGATCTGCGAGAGAGCGAGAGCTGTGCTAATGATTAATGCGAAAGCTTAATGCA 463
 QY 421 GGTTCGGTTCATCTGCTTACCGGTTTAAAGGAAACCAACCAAAAGATTGTAATTA 480
 DB 464 AGTTCGGTTCATCTGCTTACCGGTTTAAAGGAAACCAACCAAAAGATTGTAATTA 523
 QY 481 CAATATCATATCATGCGCTTAACTTAAAGCAATATTCGAAAGGCTCCGGAACCGTGG 540
 DB 524 CAATATCATATCATGCGCTTAACTTAAAGCAATATTCGAAAGGCTCCGGAACCGTGG 583
 QY 541 GTTCTCTCAATTCAGATCTCTTCTTTCACTAACGTTCTCGACGAGATGCAAGAAATGGCGG 600
 DB 584 GTTCTCTCAATTCAGATCTCTTCTTTCACTAACGTTCTCGACGAGATGCAAGAAATGGCGG 643
 QY 601 GATTAATTTTCCGGAGCGGTGACGCTCGCCCGCCGATACCTCTGTAAGTATCATGTC 660
 DB 644 GATTAATTTTCCGGAGCGGTGACGCTCGCCCGCCGATACCTCTGTAAGTATCATGTC 703
 QY 661 GAGGGTATTCAGAAACAGGAAACAGATGTGGCGCGTGGTAAAGGCCCATATATCTAT 720
 DB 704 GAGGGTATTCAGAAACAGGAAACAGATGTGGCGCGTGGTAAAGGCCCATATATCTAT 763
 QY 721 CTCAGTGAACCTTGAAGTCTTCTTTCTTCACTAACGTTCTCGACGAGATGCAATATACGTC 780
 DB 764 CTCAGTGAACCTTGAAGTCTTCTTTCTTCACTAACGTTCTCGACGAGATGCAATATACGTC 823
 QY 781 ATTGATGACATCGGACCGCATATCTTAAAGCTAAGCACTGGAAGAAATGCTGGGGCC 840
 DB 824 ATTGATGACATCGGACCGCATATCTTAAAGCTAAGCACTGGAAGAAATGCTGGGGCC 883
 QY 841 CAGAAAGATTGGCAATCAATTTGCAAGTACGTAAGCAAGTTCATTAATTAAGCGGAGATC 900
 DB 884 CAGAAAGATTGGCAATCAATTTGCAAGTACGTAAGCAAGTTCATTAATTAAGCGGAGATC 943
 QY 901 CAGCAATCTGCTTTGCAATCTGTGTAGGGGTCCAGCTTAAGAGTTCTTAAAGAA 960

DB 944 CCAGCAATCGGCTTTGCAATCTGTGTAGGGGTCCAGCTAATAAGATTCTTAGACAA 1003
 QY 961 GCAGAAATATACAGGTCTCAAGAACTGAGCTATCAAGATGAGATCTTATCACCTCACA 1020
 DB 1004 GCAGAAATATACAGGTCTCAAGAACTGAGCTATCAAGATGAGATCTTATCACCTCACA 1063
 QY 1021 GCCCCCTCTATCAAGAGAGACACAGGCAAGCCAAAGACGGGCAATCAGAAAGCCGAG 1080
 DB 1064 GCCCCCTCTATCAAGAGAGACACAGGCAAGCCAAAGACGGGCAATCAGAAAGCCGAG 1123
 QY 1081 GGT 1083
 DB 1124 GGT 1126

RESULT 4

AAT93309/c
 AAT93309 standard; DNA; 2602 BP.

AAT93309;

17-OCT-2003 (revised)

27-APR-1998 (first entry)

Tomato mottle virus full-length A-component clone.

Geminivirus; ToMoV; AC1 gene; transdominant mutation; transgenic plant;

disease resistance; ser; cyclic; circular.

Tomato mottle virus; isolate Florida.

MO9739110-A1.

23-OCT-1997.

15-APR-1997; 97WO-US006300.

16-APR-1996; 96US-0015517P.

(SEMT-) SEMINIS VEGETABLE SEEDS INC.

(WISC) WISCONSIN ALUMNI RES FOUND.

Stout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;

WPI; 1997-526447/48.

Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant

genes - have increased resistance to geminivirus infection e.g. tomato

mottle virus, tomato yellow leaf curl virus or bean golden mosaic

geminivirus.

Example 3.1; Page 76-77; 132pp; English.

This genomic DNA sequence comprises a full-length A-component clone of

tomato mottle virus (ToMoV), a geminivirus that has a bipartite genome

comprising DNA-A and DNA-B. It was isolated from ToMoV infected Nicotiana

benhamiana and tomato plant DNA by restriction digestion. The DNA-B

component (see AAT93310) was also isolated. ToMoV DNA-A contains the AC1

gene (see AAT93294) that must be expressed for efficient replication of

DNA-A and DNA-B. The invention involves production of transgenic plants

containing DNA comprising AC1 or CI wild-type or mutant sequences that

negatively interfere in trans with geminiviral replication during

infection. Such transgenic plants are resistant to viral infection.

(updated on 17-OCT-2003 to standardise OS field)

Sequence 2602 BP; 671 A; 561 C; 586 G; 784 T; 0 U; 0 Other;

Query Match 96.1%; Score 1040.8; DB 2; Length 2602;

Best Local Similarity 98.0%; Pred. No. 0;

Matches 1054; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 8 CACCAAGAAATTTAGAGTTCAATCAAGAACTATTTCTTACTTATCCCGAGTCTCTC 67

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Db      2602 CACCAAGAAATTTAGAGTTCAAGTCAAGAACTATTTCTCCTACTTATCCAGAGTCTCTT 2543
Qy      68 TATCTAAGAAGAGACATTTCCCAATTTACAAAACCTAAATACCCAGTCAACAGAAAT 127
Db      2542 TGTCTAAGAAGAGACATTTCCCAATTTACAAAACCTAAATACCCAGTCAATAGAAAT 2483
Qy      128 TCATCAAAATTTGAGAGAGCTTCATGAAAATGGGGAACCTCATCTCCATGTGCTTGTTC 187
Db      2482 TCATCAAAATTTGAGAGAGCTTCATGAAAATGGGGAACCTCATCTCCATGTGCTTGTTC 2423
Qy      188 AGTTGGAAGGTAAGTACCAATGACAGATAACAGATTCTTCGACTGCTGCTCCCAACC 247
Db      2422 AGTTGGAAGGTAAGTACCAATGACAGATAACAGATTCTTCGACTGCTGCTCCCAACC 2363
Qy      248 GGTGAGACATTTTCATCCGAAATTTTCAGGGAGCTAAATCGAGCTCCGAGCTCAATCAT 307
Db      2362 GGTGAGACATTTTCATCCGAAATTTTCAGGGAGCTAAATCGAGCTCCGAGCTCAATCAT 2303
Qy      308 ACATCGACAGAGAGAGATTCATTCGAAATGGGGAATTTCCAAATCGAGCGAGATCTG 367
Db      2302 ACATCGACAGAGAGAGATTCATTCGAAATGGGGAATTTCCAAATCGAGCGAGATCTG 2243
Qy      368 CCAGAGAGGCGCAGAGCTGCTATGATTCATTAATGAGAAAGCATTAATGACAGTTCGG 427
Db      2242 CCAGAGAGGCGCAGAGCTGCTATGATTCATTAATGAGAAAGCATTAATGAGATTCGG 2183
Qy      428 TTCAATCTGCTTAGCGGTTCTAAGGAGAGAACCAACAAAGATTTGTATTAACAAATC 487
Db      2182 TTCAATCTGCTTAGCGGTTCTAAGGAGAGAACCAACAAAGATTTGTATTAACAAATC 2123
Qy      488 ATAACATCCGCTCTAACCCTAGAAAGAAATTTTCGAAAGGCTCCGAAACCTGGGTTCTC 547
Db      2122 ATAACATCCGCTCTAACCCTAGAAAGAAATTTTCGAAAGGCTCCGAAACCTGGGTTCTC 2063
Qy      548 CATTTCAAGTCTCTTTCTTCACTAACGTTCTCTGACGATGACAGAAATGGGCGGATTAAT 607
Db      2062 CATTTCAAGTCTCTTTCTTCACTAACGTTCTCTGACGATGACAGAAATGGGCGGATTAAT 2003
Qy      608 ATTTCCGGAGCGGTGACGCTGCGCGCGCGAGTAGACCTGTAAATCATCGTCGAGGGTG 667
Db      2002 ATTTCCGGAGCGGTGACGCTGCGCGCGCGAGTAGACCTGTAAATCATCGTCGAGGGTG 1943
Qy      668 ATTCAAGAAACAGGAAACAGATGTGGGCGGTGTTAGCCCACTAATCATCTCAGTG 727
Db      1942 ATTCAAGAAACAGGAAACAGATGTGGGCGGTGTTAGCCCACTAATCATCTCAGTG 1883
Qy      728 GACACCTAGACTTCAATGAGTGCAGTCTTCTCGAATGATGTGCAGTATTAACGTCAATTG 787
Db      1882 GACACCTAGACTTCAATGAGTGCAGTCTTCTCGAATGATGTGCAGTATTAACGTCAATTG 1823
Qy      788 ACATCGACCGCATTTATCTAAAGCTAAAGCACTGAAAAGAAATTCCTGGGGGCCAGAAAG 847
Db      1822 ACATCGACCGCATTTATCTAAAGCTAAAGCACTGAAAAGAAATTCCTGGGGGCCAGAAAG 1763
Qy      848 ATTGGCAATCAAAATTTGCAAGTACGTAAGCCAGTTCAAAATTAAGGGGGAATCCACAG 907
Db      1762 ATTGGCAATCAAAATTTGCAAGTACGTAAGCCAGTTCAAAATTAAGGGGGAATCCACAG 1703
Qy      908 TCGTCTTTGCAATCTGCTGAGGGGTCCAGCTTAAGAAGTTTGAACAAACAGAGAA 967
Db      1702 TCGTCTTTGCAATCTGCTGAGGGGTCCAGCTTAAGAAGTTTGAACAAACAGAGAA 1643
Qy      968 ATACAGGTTCAAGAACTGGAATATCAAGAAATGGGATCTTCATGACCTTCACAGCCCCC 1027
Db      1642 ATACAGGTTCAAGAACTGGAATATCAAGAAATGGGATCTTCATGACCTTCACAGCCCCC 1583
Qy      1028 TCATATCAAGAGACACAGGCAAGCAAGAAACGGGCATTCAGAAAGCGGAGGT 1083
Db      1582 TCATATCAAGACAGACACAGGCAAGCAAGAAACGGGCATTCAGAAAGCGGAGGT 1527

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ID      AAT93282 standard; DNA; 1169 BP.
XX
XX      AAT93282;
AC
XX      27-Apr-1998 (first entry)
DT
XX      Tomato mottle virus AC1 mutant Tomov-Acidim gene.
DE
XX      Geminiivirus; Tomov-Acidim; AC1 gene; transdominant mutation;
XX      transgenic plant; disease resistance; ss; cyclic; circular.
KM
XX      Tomato mottle virus; isolate Florida.
OS
XX      Synthetic.
FH
XX      Key
FT      CDS
FT      Location/Qualifiers
FT      44..1129
FT      /*tag= a
XX
XX      MO9739110-A1.
PN
XX      23-OCT-1997.
XX
XX      15-APR-1997; 97MO-US006300.
XX
XX      16-APR-1996; 96US-0015517P.
PR
XX      (SEMI-) SEMINIS VEGETABLE SEEDS INC.
PA      (WISC-) WISCONSIN ALUMNI RES FOUND.
XX
XX      Scout UT, Luu HT, Hanson SR, Maxwell DP, Ahlquist PG;
PI      WPI; 1997-526447/48.
DR      P-PSDB; AAW34324.
XX
XX      Transgenic plants expressing geminiivirus AC1 and CI wild-type and mutant
PT      genes - have increased resistance to geminiivirus infection e.g. tomato
PT      mottle virus, tomato yellow leaf curl virus or bean golden mosaic
PT      geminiivirus.
XX
XX      Claim 11; Page 60-62; 132p; English.
XX
XX      This DNA sequence comprises a transdominant lethal mutant, designated
CC      Tomov-Acidim, of the AC1 gene of tomato mottle virus (Tomov). It
CC      encodes an AC1 protein (see AAW34324) that carries mutations in its NTP-
CC      binding domains. The AC1 gene (see also AAT93294) must be expressed for
CC      efficient replication of the two genomic components, DNA-A and DNA-B, of
CC      the bipartite Tomov genome. The invention involves production of
CC      transgenic plants containing DNA comprising geminiivirus AC1 or CI wild-
CC      type or mutant sequences that negatively interfere in trans with
CC      geminiiviral replication during infection. Such transgenic plants are
CC      resistant to viral infection. The AC1/CI genes are especially from Tomov,
CC      tomato yellow leaf curl virus or bean golden mosaic geminiivirus (see
CC      AAT93282-93) and encode polypeptides (see AAW34324-35) that have
CC      mutations in the highly conserved DNA-nicking and/or the NTP-binding
CC      domains
XX
XX      Sequence 1169 BP; 363 A; 281 C; 255 G; 270 T; 0 U; 0 Other;
SQ

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Query Match 95.9%; Score 1038.2; DB 2; Length 1169;
 Best Local Similarity 97.4%; Pred. No. 0;
 Matches 1055; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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Qy      1 ATGCCCCCACCAGAAATTTAGAGTTCAAGTCAAGAACTAATTTCTCACTAATCCAG 60
Db      44 ATGCCCCCACCAGAAATTTAGAGTTCAAGTCAAGAACTAATTTCTCACTAATCCAG 103
Qy      61 TGTCTCTATCTAATAAGAGACATTTCCCAATTAACAAACCTAAATACCCAGTCAAC 120
Db      104 TGTCTCTTGTCTAATAAGAGACATTTCCCAATTAACAAACCTAAATACCCAGTCAAT 163
Qy      121 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAATAATGGGGAACCTCATCTCAGTG 180
Db      164 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAATAATGGGGAACCTCATCTCAGTG 223

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QY 181 CTTGTTCAGTTCGAAGGTAAGTACCAATGCAAGATAACAGATTCTTGCAGCTGTCTCC 240
Db 224 CTTGTTCAGTTCGAAGGTAAGTACCAATGCAAGATAACAGATTCTTGCAGCTGTCTCC 283
QY 241 CCAACCCGGTGCAGACATTTTCATCCGAATATTCAGGAGGTAAATCGAGTCCGAGTC 300
Db 284 CCAACCCGGTGCAGACATTTTCATCCGAATATTCAGGAGGTAAATCGAGTCCGAGTC 343
QY 301 AAATCATCATCGACAAAGACGAGATCAATTCGATGGGAGATTTTCAATCGACGGC 360
Db 344 AAATCGTACATCGACAAAGACGAGATCAATTCGATGGGAGATTTTCAATCGACGGC 403
QY 361 AGATCTGCAGAGAGGCGACGACTGCTATATTCATTTGGGAAAGCAATTAATGCA 420
Db 404 AGATCTGCAGAGAGGCGACGACTGCTATATTCATTTGGGAAAGCAATTAATGCA 463
QY 421 GGTTCGGTTCATCTGCTTAGCGGTTCTAAGGGAAGAACCAAAAGATTTTGTATTA 480
Db 464 AGTTCGGTTCATCTGCTTAGCGGTTCTAAGGGAAGAACCAAAAGATTTTGTATTA 523
QY 481 CAAATCATTAATCCGCTCTAACCCTAGAACGAATATTCGAAAGGCTCCGAAACGCTGG 540
Db 524 CAAATCATTAATCCGCTCTAACCCTAGAACGAATATTCGAAAGGCTCCGAAACGCTGG 583
QY 541 GTTCTCCATTTCAAGTCTCTTTTCACTAAGCTTCTGACGAGATGCAAGAAATGGGCG 600
Db 584 GTTCTCCATTTCAAGTCTCTTTTCACTAAGCTTCTGACGAGATGCAAGAAATGGGCG 643
QY 601 GATTAATTAATTCGGGACGGGTGACGCTGCGCGCGAGTAGACCTGTAAAGTATCATCTC 660
Db 644 GATTAATTAATTCGGGACGGGTGACGCTGCGCGCGAGTAGACCTGTAAAGTATCATCTC 703
QY 661 GAGGCTGATTTAAAGAACGGGAAGACATGTGGGCGCGCTGTTAGGCCCAATTAATCTAT 720
Db 704 GAGGCTGATTTAAAGAACGGGACACGATGTGGGACGCTGTTAGGCCCAATTAATCTAT 763
QY 721 CTCAGTGGACACCTAGACTTCAATGTGTGAGTCTTTCTGGAATGATGTGCAATTAATGCTC 780
Db 764 CTCAGTGGACACCTAGACTTCAATGTGTGAGTCTTTCTGGAATGATGTGCAATTAATGCTC 823
QY 781 ATTGATGACATCGACCGCATTTATCTAAAGCTAAAGCACTGGAAGAATGCTGGGGGCC 840
Db 824 ATTAAATACATCGACCGCATTTATCTAAAGCTAAAGCACTGGAAGAATGCTGGGGGCC 883
QY 841 CAGAAAGATTGGCAATCAAAATGCAAGTACGCTAAGCCAGTTCAATTAAGGCGGAATC 900
Db 884 CAGAAAGATTGGCAATCAAAATGCAAGTACGCTAAGCCAGTTCAATTAAGGCGGAATC 943
QY 901 CCAGCAATCGTGTCTTTGCAATCTGTGTAGGGGTGCGAGCTATTAAGAAGTCTTGTAGACAA 960
Db 944 CCAGCAATCGTGTCTTTGCAATCTGTGTAGGGGTGCGAGCTATTAAGAAGTCTTGTAGACAA 1003
QY 961 GCAGAAAATTAAGGTTCTCAAGAACTGCACTATCAAGAAATGCGATCTTTCATCACTCCACA 1020
Db 1004 GCAGAAAATTAAGGTTCTCAAGAACTGCACTATCAAGAAATGCGATCTTTCATCACTCCACA 1063
QY 1021 GCCCCCTCTTCAAGAGAGACACCAAGCCAAAGAAAGGGCAATCAGAAGGCGAG 1080
Db 1064 GCCCCCTCTTCAAGAGAGACACCAAGCCAAAGAAAGGGCAATCAGAAGGCGAG 1123
QY 1081 GGT 1083
Db 1124 GGT 1126

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RESULT 6
AAT93285
ID AAT93285 standard; DNA; 1166 BP.

AC AAT93285;
XX
DT 27-APR-1998 (first entry)

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XX DE Tomato mottle virus AC1 mutant gene.
XX DE Geminivirus; ToMoV-Acid1m23; AC1 gene; transdominant mutation;
XX KM transgenic plant; disease resistance; ss; cyclic; circular.
XX OS Tomato mottle virus; isolate Florida.
XX OS Synthetic.
XX FH
XX FT Key
XX FT CDS
XX FT Location/Qualifiers
XX FT 44..439
XX FT /*tag= a
XX PN MO9739110-A1.
XX PD 23-OCT-1997.
XX XX
XX PF 15-APR-1997; 97MO-US006300.
XX PR 16-APR-1996; 96US-0015517P.
XX XX
XX PA (SEMT-) SEMINIS VEGETABLE SEEDS INC.
XX PA (WISC ) WISCONSIN ALUMNI RES FOUND.
XX PI Stout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;
XX DR WP1: 1997-526447/48.
XX DR P-PSDB; AAW34327.
XX XX
XX PT Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
XX PT genes - have increased resistance to geminivirus infection e.g. tomato
XX PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic
XX PT geminivirus.
XX PS Claim 11; Page 72-73; 132pp; English.
XX XX
XX CC This DNA sequence comprises a mutated AC1 gene of tomato mottle virus
XX CC (ToMoV). It carries an inserted 4-base Sau3A site that shifts the AC1
XX CC gene translation reading frame resulting in the expression of a truncated
XX CC AC1 protein (see AAW34327). The AC1 gene (see also AAT93294) must be
XX CC expressed for efficient replication of the two genomic components, DNA-A
XX CC and DNA-B, of the bipartite ToMoV genome. The invention involves
XX CC production of transgenic plants containing DNA comprising geminivirus AC1
XX CC or CI wild-type or mutant sequences that negatively interfere in trans
XX CC with geminiviral replication during infection. Such transgenic plants are
XX CC resistant to viral infection. The AC1/CI genes are especially from ToMoV,
XX CC tomato yellow leaf curl virus or bean golden mosaic geminivirus (see
XX CC AAT93282-93) and encode polypeptides (see AAW34324-35) that have
XX CC mutations in the highly conserved DNA-nicking and/or the NTP-binding
XX CC domains
XX SO
XX
XX Sequence 1166 BP; 361 A; 277 C; 260 G; 268 T; 0 U; 0 Other;
XX
XX Query Match 95.5%; Score 1033.8; DB 2; Length 1166;
XX Best Local Similarity 97.6%; Pred. No. 0;
XX Matches 1061; Conservative 0; Mismatches 22; Indels 4; Gaps 1;
XX
XX QY 1 ATGCCCCCACCAGAAATTTAGAGTCAAGTCAAGAAAGCAATTTCCATCTATCCCAAG 60
XX Db 44 ATGCCCCCACCAGAAATTTAGAGTCAAGTCAAGAAAGCAATTTCCATCTATCCCAAG 103
XX
XX QY 61 TGCTCTATCTAAAGAAAGACCTTCCCAATTAACAAACCTAATACCCAGTCAAC 120
XX Db 104 TGCTCTATCTAAAGAAAGACCTTCCCAATTAACAAACCTAATACCCAGTCAAT 163
XX
XX QY 121 AAGAAATTCATCAAAATTTTCAGAGAGCTTCATGAAAAATGAGGAAACCTCATCTTCATGTG 180
XX Db 164 AAGAAATTCATCAAAATTTTCAGAGAGCTTCATGAAAAATGAGGAAACCTCATCTTCATGTG 223
XX
XX QY 181 CTTGTTCAGTTCGAAGGTAAGTACCAATGCAAGATAACAGATTCTTGCAGCTGTCTCC 240
XX Db 224 CTTGTTCAGTTCGAAGGTAAGTACCAATGCAAGATAACAGATTCTTGCAGCTGTCTCC 283

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QY	241	CCAAACCGGGTGA	GACATTTCCATCGCAATATTTACAGGGAGCTAAATCGAGCTCCGACGTC	300
Db	284	CCAAACCGGGTGA	GACATTTCCATCGCAATATTTACAGGGAGCTAAATCGAGCTCCGACGTC	343
QY	301	AAATCATATCAT	CGACAGGACGGAGATCAATCGAATGGGGAGATTTCCAAATCGACGGC	360
Db	344	AAATCGTATCAT	CGACAGGAGGAGATCAATCGAATGGGGAGATTTCCAGATCGACGGC	403
QY	361	A----	GATCTGCGAGAGAGGCGCAGCAGTCTGCTAATGATTCATATGCGAAAGCATTA	416
Db	404	AGATCGATCTG	CAGAGGAGCGCAGCAGTCTGCTAATGATTCATATGCGAAAGCGTTAA	463
QY	417	TGCAAGTTCCG	GTTCATCTGCTTACGCGCTTACGCGCTTACGCGGAAACCAAAAGATTTTGT	476
Db	464	TGCAAGTTCCG	GTTCATCTGCTTACGCGCTTACGCGGAAACCAAAAGATTTTGT	523
QY	477	ATTACAAATCAT	ATACATCCGCTCTAACCTTAGAACGAATATTGCAAAAGGCTCCGAAAC	536
Db	524	ATTACAAATCAT	ATACATCCGCTCTAACCTTAGAACGAATATTGCAAAAGGCTCCGAAAC	583
QY	537	GTGGGTTCTC	TCATTTCAAGTCTCTTTCTTCACTAACGTTCTCGACGAGATGACGAATG	596
Db	584	GTGGGTTCTC	TCATTTCAAGTCTCTTTCTTCACTAACGTTCTCGACGAGATGACGAATG	643
QY	597	GGCGGATTAAT	TATTTTCGGGACGGGTGACGCTCGCGCGCGGATGACCTGTAAAGTATCAT	656
Db	644	GGCGGATTAAT	TATTTTCGGGACGGGTGACGCTCGCGCGGATGACCTGTAAAGTATCAT	703
QY	657	CGTCGAGGGTGA	TTCAAGAACGAGGAAGCAGATGTGTGGCGCGTGTGGGCCCATTA	716
Db	704	CGTCGAGGGTGA	TTCAAGAACGAGGAAGCAGATGTGTGGCACGTGCTTTAGGCCCATTA	763
QY	717	CTATCTCAGTGA	CACTAGACTTCAATGTCGAGTCTTCTCGAATGATGTGCAATATA	776
Db	764	CTATCTCAGTGA	CACCTTAGACTTCAATGTCGAGTCTTCTCGAATGATGTGCAATATA	823
QY	777	CGTCTTTGATGA	CATTCGCAACCGGCATTTATTTAAAGCTTAAGCACTGGAAAGATTTGCTGGG	836
Db	824	CGTCTTTGATGA	CATTCGCAACCGGCATTTATTTAAAGCTTAAGCACTGGAAAGATTTGCTAGG	883
QY	837	GGCCCGAAGAA	GGTGTGGCAATCAAAATTGCAAGTACGGTAAAGCCAGTCAAAATTTAAAGCGG	896
Db	884	GGCCCGAAGAA	GGTGTGGCAATCAAAATTGCAAGTACGGTAAAGCCAGTCAAAATTTAAAGCGG	943
QY	897	AATCCAGCAAT	CGTGTCTTTGGCAATCTGTGTGAGGGGTGCGAGCTATTAAGAGTTCTTAGA	956
Db	944	AATCCAGCAAT	CGTGTCTTTGGCAATCTGTGTGAGGGGTGCGAGCTATTAAGAGTTCTTAGA	100
QY	957	CAAGCAGAAAT	TACAGGTCCTCAAGAACTGACCTATCAAGAATGCGATCTTCAACCTT	101
Db	1004	CAAGCAGAAAT	TACAGGTCCTTAAAGAACTGACCTTCAAGAATGCGATCTTCAACCTT	106
QY	1017	CACAGCCCCCT	CTATTCAGAGAGACACACAGCAAGCCCAAGAAACGGGCAATTCAGAAAGC	107
Db	1064	CACAGCCCCCT	CTATTCAGAGAGACACACAGCAAGCAAGCCCAAGAAACGGGCAATTCAGAAAGC	112
QY	1077	GCAGGGT	1083	
Db	1124	GCAGGGT	1130	
RESULT 7				
AAT93286				
ID AAT93286 standard; DNA; 1246 BP.				
AC	AAT93286;			
XX				
DT	17-OCT-2003 (revised)			
DT	27-APR-1998 (first entry)			
XX				
DE	Tomato mottle virus AC1-AC2-AC3 DNA.			
XX				
XX	Geminivirus; Tomato-Acidim; AC1 gene; transdominant mutation;			

Accession	Sequence	Query Match	Best Local Similarity	Matches
XX XX	transgenic plant; disease resistance; ss; cylic; circular.			
XX XX	Tomato mottle virus; isolate Florida.			
XX XX	WO9739110-A1.			
XX XX	23-OCT-1997.			
XX XX	15-APR-1997; 97WO-US006300.			
XX XX	16-APR-1996; 96US-0015517P.			
XX XX	(SEMI-) SEMINIS VEGETABLE SEEDS INC.			
XX XX	(WISC) WISCONSIN ALUMNI RES FOUND.			
XX XX	Stout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;			
XX XX	WPI; 1997-526447/48.			
XX XX	Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant			
XX XX	genes - have increased resistance to geminivirus infection e.g. tomato			
XX XX	mottle virus, tomato yellow leaf curl virus or bean golden mosaic			
XX XX	geminivirus.			
XX XX	Claim 11; Page 75; 132pp; English.			
XX XX	This DNA sequence comprises the complete AC2 and AC3 coding sequences and			
XX XX	the C-terminal two-thirds of the AC1 open reading frame (see also			
XX XX	AA993294) of tomato mosaic virus (ToMoV). It was obtained by ligating a			
XX XX	BamHI-HindIII fragment of a binary plasmid composed of a dimer of the			
XX XX	full-length, infectious ToMoV A-component with BamHI-HindIII-digested			
XX XX	pUTS222, inserting a BamHI-HindIII fragment of this construct into			
XX XX	pBlueScript II KS+, and digesting with BglI and SphI. The AC1 gene must			
XX XX	be expressed for efficient replication of the two genomic components, DNA			
XX XX	-A and DNA-B, of the bipartite ToMoV genome. The invention involves			
XX XX	production of transgenic plants containing DNA comprising geminivirus AC1			
XX XX	or CI wild-type or mutant sequences that negatively interfere in trans			
XX XX	with geminiviral replication during infection. Such transgenic plants are			
XX XX	resistant to viral infection. The AC1/CI genes are especially from ToMoV,			
XX XX	tomato yellow leaf curl virus or bean golden mosaic geminivirus (see			
XX XX	AA993292-93) and encode polypeptides (see AA93324-35) that have			
XX XX	mutations in the highly conserved DNA-nicking and/or the NTP-binding			
XX XX	domains. (Updated on 17-OCT-2003 to standardise OS field)			
XX XX	Sequence 1246 BP; 393 A; 264 C; 284 G; 305 T; 0 U; 0 Other;			
XX XX	Query Match 64.8%; Score 702.2; DB 2; Length 1246;			
XX XX	Best Local Similarity 98.2%; Pred. No. 1.7e-212;			
XX XX	Matches 710; Conservative 0; Mismatches 13; Indels 0; Gaps 0			
XX XX	361 AGATCTGCAGAGGAGGCGCAGACAGTCTGCTATGATTCATATGCGAAGCATTAATCA 420			
XX XX	1 AGATCTGCAGAGGAGGCGCAGACAGTCTGCTATGATTCATATGCGAAGCATTAATCA 60			
XX XX	421 GGTTCGTTCAATCTGCTTATGCGGTTCTAAGGAAAGCAACCAAAAGATTTGTATTA 480			
XX XX	61 AGTTCGTTCAATCTGCTTATGCGGTTCTAAGGAAAGCAACCAAAAGATTTGTATTA 120			
XX XX	481 CAAATATCAATCAATCCGCTCTAACCCTGAAGCAATATTCGGAAGAGCTCCGGAACCGG 540			
XX XX	121 CAAATATCAATCAATCCGCTCTAACCCTGAAGCAATATTCGGAAGAGCTCCGGAACCGG 180			
XX XX	541 GTTCCTCATTTCAAGTCTCTTTCTTCACTAAGCTTCTCTGACGAGATGACGAATGGCG 600			
XX XX	181 GTTCCTCATTTCAAGTCTCTTTCTTCACTAAGCTTCTCTGACGAGATGACGAATGGCG 240			
XX XX	601 GATTAATTAATTCGGAAGCGGTGACGCTGCGCGCGGATAGACCTGTATGATCATCGTC 660			
XX XX	241 GATTAATTAATTCGGAAGCGGTGACGCTGCGCGCGGATAGACCTGTATGATCATCGTC 300			
XX XX	661 GAGGCTATTCGAAGCAAGGGAAGACATATGAGGCGGTGCTTAAGGCCCATTAACAT 720			
XX XX	301 GAGGCTATTCGAAGCAAGGGAAGACATATGAGGCGGTGCTTAAGGCCCATTAACAT 360			

QY 721 CTGAGTGAACACCTAGACTTCAATGTCGAGTCTTTCGATGATGATGTCAGTATTAAGTC 780
DB 361 CTCAGTGAACACCTAGACTTCAATGTCGAGTCTTTCGATGATGATGTCAGTATTAAGTC 420
QY 781 ATTGATGACATCGACCGCATTTATCTAAAGCTGAAGCACTGGAAGAATTCCTGGGGCC 840
DB 421 ATTGATGACATCGACCGCATTTATCTAAAGCTGAAGCACTGGAAGAATTCCTGGGGCC 480
QY 841 CAGAAAGATTGGCAATCAATTTGCAAGTACCGTAAAGCCAGTTCAATTAAGCGGGAATC 900
DB 481 CAGAAAGATTGGCAATCAATTTGCAAGTACCGTAAAGCCAGTTCAATTAAGCGGGAATC 540
QY 901 CCAGCAATCGTCTGCAATCCGTGTAGGGGTCCAGCTATTAAGAGTTCTTAGACAA 960
DB 541 CCAGCAATCGTCTGCAATCCGTGTAGGGGTCCAGCTATTAAGAGTTCTTAGACAA 600
QY 961 GCAGAAATACAGGTCTCAAGACCTGACATCAAGATGCGATCTTCAATCCCTGACA 1020
DB 601 GCAGAAATACAGGTCTCAAGACCTGACATCAAGATGCGATCTTCAATCCCTGACA 660
QY 1021 GCGCCCTCTATCAAGAGACACACAGGCAAGCCAGAAACGGCAATCAGAGGGCGAG 1080
DB 661 GCGCCCTCTATCAAGAGACACACAGGCAAGCCAGAAACGGGCAATCAGAGGGCGAG 720
QY 1081 GGT 1083
DB 721 GGT 723

RESULT 8
AAT93314
ID AAT93314 standard; DNA; 1183 BP.

AC AAT93314;
XX 17-OCT-2003 (revised)
DT 27-APR-1998 (first entry)
XX

DE Bean golden mosaic geminivirus CI open reading frame.

XX Geminivirus; BGMV; CI gene; transdominant mutation; transgenic plant;
KM disease resistance; ss; cyclic; circular.

XX Bean golden mosaic virus; type II isolate Guatemala.

OS
FH Key Location/Qualifiers
FT CDS 1..1062
FT /tag= a

XX W09739110-A1.

XX 23-OCT-1997.

XX 15-APR-1997; 97WO-US006300.

XX 16-APR-1996; 96US-0015517P.

XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.

XX (WISC) WISCONSIN ALUMNI RES FOUND.

XX Scout JT, Lau HT, Hanson SF, Maxwell DP, Ahlquist PG;

XX WPI; 1997-526447/48.

XX P-PSDB; AAM34338.

XX Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
PT genes - have increased resistance to geminivirus infection e.g. tomato
PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic
PT geminivirus.

XX Example 5; Page 100-102; 132p; English.

CC This genomic DNA sequence includes the open reading frame (ORF) of the
CC wild-type CI gene of bean golden mosaic virus (BGMV), a geminivirus that
CC has a monopartite genome. The CI protein (see AAT93314) is required for
CC replication. The wild-type CI ORF was subjected to Kunkel mutagenesis
CC (see AAT93290-93). The invention involves production of transgenic plants
CC containing DNA comprising CI or AC1 wild-type or mutant sequences that
CC negatively interfere in trans with geminiviral replication during
CC infection. Such transgenic plants are resistant to viral infection. The
CC AC1/CI genes are especially from BGMV, tomato mottle virus or tomato
CC yellow leaf curl virus (see AAT93282-93) and encode polypeptides (see
CC AAT93432-35) that have mutations in the highly conserved DNA-nicking
CC domain and/or the NTP-binding domains. (Updated on 17-OCT-2003 to
CC standardise OS field)

XX Sequence 1183 BP; 372 A; 276 C; 248 G; 287 T; 0 U; 0 Other;

Query Match 64.3%; Score 696.2; DB 2; Length 1183;
Best Local Similarity 77.9%; Pred. No. 1.3e-210;
Matches 839; Conservative 0; Mismatches 238; Indels 0; Gaps 0;

QY 1 ATGCCCCACCAAGAAATTTAGATGATCAAGAACTATTTCCACTTATCCCCAG 60
DB 1 ATGCAACACCTCAAGATTTAGATGATCAAGAACTATTTCCACTTATCCCTGT 60
QY 61 TGCTCTATCTAAAGAAAGCACTTCCCAATTACAAACCTTAATACCCAGTCAAC 120
DB 61 TGCCCTATACGAAGAAAGAAAGTTCTTCCCACTTCAAGAAATTCATACGACGAAT 120
QY 121 AAGAAATTCATCAAAATTTGCAAGAGCTTCATGAAGAAATGGGAACTCATCTCATGTG 180
DB 121 AAAAAATTCATCAAAAGCTGTGAGGAACGTACAGAGAAATGGTGAACCTCATCTTCATGCG 180
QY 181 CTGTGATGTCGAAGTAAAGTACCAATGACGAATTAAGATTTCTTCGACCTGGTCC 240
DB 181 CTATTAATTCGAAGTAAATGCTGTGAGGAACGTACAGAGAAATGGTGAACCTCATCTTCATGCG 240
QY 241 CCAACCCGTCAGACATTTCCATCCGATATTTCAAGGAGCTTAATGAGCTCCGACGTC 300
DB 241 TCAACGAGTCAAGACCTTTCCATCCGATATTTCAAGGAGCTTAATGAGTTCAGACGTC 300
QY 301 AATATCATCATCGAAGAAAGACGAGATTAATGATGAGGAGATTTCCAAATGACGCG 360
DB 301 AAGGCAATCATCGAAGAAAGATGAGTCAATGCAATGAGGAGACATTTCCAAGTCGACGCG 360
QY 361 AGATCGCCAGAGAGGCGCAGCTGCTTAATGATTCATATGAGGAAAGATTAATGCA 420
DB 361 AGATCTGAAGAGAGGTCAGAGTGTGCAACGACTCATATGAGGAAAGCAATTAACGCA 420
QY 421 GGTTCGTTCAATCTGCTTAGCGGTTCTTAAGGGAAGAACCAACCAAAAGATTTGTATTA 480
DB 421 GATTCAATGATCTGCTTGACATATTTGAAGGAAGAACCAACCAAAAGATTTAGTCTT 480
QY 481 CAAAATCATTAATCGCTCTTAACCTTAAGAAAGAAATTTCCAAAGCTCCGGAACGCTGG 540
DB 481 CAACATCAAAATCCCTTCTTAATCTGAAACGATCTTCTCAAAAGCGCGGAACCAATGG 540
QY 541 GTTCCTCATTTCAAGTCTCTTCTTCACTAAGTCTCTGACGAGATGAGAGTGGCG 600
DB 541 GTTCCTCATTTCCGTGTCTATCTATCAATGATTTCCGTTGTATGCAAGAAATGGGTT 600
QY 601 GATTAATTTTCGGAGCGGTTGACGCTGCGCCGCGGATAGACTGTAGTATCATGTC 660
DB 601 GAGCACTATTTTCGGAAGGGTTCCGCTGCGCGCGCGGAAGAACTTATGATCATGTC 660
QY 661 GAGGTCATTTCAAGAACAGGAAGACATGTGGCGGCTGCTTAGGCCCACTAATCTAT 720
DB 661 GAAGGTATTTCAAGAACAGGAAGACATGTGGGCTGTGCAATTAAGAACACATTAAT 720
QY 721 CTGAGTGAACACCTAGACTTCAATGTCGAGTCTTTCGATGATGATGTCAGTATTAAGTC 780
DB 721 TTGAGCGGTCATTTGACCTTAAATTCACGTCGTCTAATTCACGAGTGGAAATACAGTC 780
QY 781 ATTGATGACATCGACCGCATTTATCTAAAGCTGAAGCACTGGAAGAATTCCTGGGGCC 840

OS Synthetic.
 XX US618048-A.
 PN 12-SEP-2000.
 PD XX
 PF 24-APR-1998; 98US-0006599.
 XX
 PR 25-APR-1997; 97US-0044925P.
 XX
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 XX Maxwell DP, Hanson SF;
 PI MPI; 2000-610861/58.
 DR
 XX
 PT Genetic construct comprising a mutant geminiviral rep gene, useful for
 PT producing a plant resistant to geminiviral infection.
 XX
 PS Example; Col 17-20; 14pp; English.
 XX
 PS The present sequence is pTrep23. It contains the wild type geminivirus
 CC rep gene sequence. Genetic constructs containing DNA-nicking domain
 CC mutants in the rep gene may be used as trans-dominant inhibitors of
 CC geminiviral replication. When expressed in a plant cell, these inhibitors
 CC are able to dramatically reduce replication of geminivirus. Genetic
 CC constructs that include sequences containing a portion of the ac3 gene in
 CC addition to the trans-dominant inhibitor exhibit increased efficiency and
 CC broadened specificity of inhibition of geminiviral replication.
 CC Geminiviruses are one of the greatest constraints on production of
 CC important crops, including cassava, beans, cowpeas, peppers, tomatoes and
 CC cotton. The effects of the virus can be overcome by using the genetic
 CC construct
 XX
 SQ Sequence 2072 BP; 661 A; 467 C; 421 G; 523 T; 0 U; 0 Other;
 Query Match 64.3%; Score 696.2; DB 3; Length 2072;
 Best Local Similarity 77.9%; Pred. No. 1.8e-210;
 Matches 839; Conservative 0; Mismatches 238; Indels 0; Gaps 0;

DB 949 CAACATCACAAACCTCGTTCTAATCTCGAAGCATCTTGTCTCAAATGCTCCGGAACCATGG 1008
 QY 541 GTTCTCTCAATTCAGAGTCTTCTTCTCACTAAAGTCTGTAGAGAGATGAGAAATGGCGC 600
 DB 1009 GTTCTCTCAATTCAGAGTCTTCTTCTCACTAAAGTCTGTAGAGAGATGAGAAATGGCGC 1068
 QY 601 GATTAATTAATTTGGAGCGGCTGACGCTGCGCGCGGATGAGACCTGTAAATGATATGCTC 660
 DB 1069 GACGACTAATTTGCGAAGGGGTTCCGCTGCGCGCGCGGAAAGACCTAATTAATGATATGCTC 1128
 QY 661 GAGGATGATTCAGAAAGAGAGAGAGATGAGGCGGCGGCTGAGGCCACATACTAT 720
 DB 1129 GAAGGATTCAGAAAGAGAGAGAGATGAGGCGGCGGCTGAGGCCACATACTAT 1188
 QY 721 CTCAGTGAACACCTAGACTTCAATGCTGAGAGTCTTCTGAAATGATGAGATGAAAGTTC 780
 DB 1189 TTGAGCGGCTCATTTGAGACTTTAATTCACGTTCTATTCACAGCAGTGGAAATCAAGTTC 1248
 QY 781 ATTGATGACATGCGACCGCATTTCTTAAAGCTTAAGCACTGGAAGAAATGCTGGGGCC 840
 DB 1249 ATTGATGACATTAAGCCCAATTAATTTGAAGTTAAAGCACTGGAAGAAATGCTGGGGCC 1308
 QY 841 CAGAAGATTTGCAATCAATTCAGATGAGTACGCTGAGGCGGCTGCAATTAAGGCGGAATC 900
 DB 1309 CAAAGGACTGCGCAATCTAATCTTAATTAATTAAGGCGGCTGCAATTAAGGCGGAATC 1368
 QY 901 CCAGCATGCTGCTTTCAGATCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 960
 DB 1369 CATCAATGCTGCTTTCAGATCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1428
 QY 961 GCGAATAATCAAGTCTCAAGAACTGAGTATCAAGATGCGATCTTCAATACCTTCACA 1020
 DB 1429 GAAGAAACCGAGCTTTACACAACTGAGTATCAATTAAGCGATCTTCCGTCACCTCACA 1488
 QY 1021 GCCCCCTCTATCAAGAGACACAGGCAAGGCAAGAAAGCGGCAATCAAGAGGGG 1077
 DB 1489 GCCCCCTCTATCAAGAGACACAGGCAAGGCAAGAAAGCGGCAATCAAGAGGGG 1545

RESULT 12
 AAT933290
 ID AAT93290 standard; DNA; 1183 BP.
 XX
 AC AAT933290;
 XX
 DT 17-OCT-2003 (revised)
 DT 27-APR-1998 (first entry)
 XX
 DE Bean golden mosaic geminivirus CI mutant gene.
 XX
 KM Geminivirus; BGMV; CI gene; transdominant mutation; transgenic plant;
 KM disease resistance; ss; cyclic; circular.
 XX
 OS Bean golden mosaic virus; type II isolate Guatemala.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1062
 FT /*tag= a
 XX
 PN W09739110-A1.
 XX
 PD 23-OCT-1997.
 XX
 PF 15-APR-1997; 97MO-US006300.
 PF
 PR 16-APR-1996; 96US-0015517P.
 XX
 XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 XX
 PI Scout UT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;

DR WPI; 1997-526447/48.
 DR P-PsDB; AAM34332.
 XX Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
 PT genes - have increased resistance to geminivirus infection e.g. tomato
 PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic
 PT geminivirus.
 XX
 PS Claim 13; Page 103-105; 132pp; English.
 CC This DNA sequence comprises construct BGAC190 that codes for a control
 CC mutant (see AAM34332) of the CI protein (see AAM34338) of bean golden
 CC mosaic virus (BGWV). It was obtained by Kunkel mutagenesis of the wild-
 CC type CI gene (see AAT9314). CI is required for replication. The
 CC invention involves production of transgenic plants containing DNA
 CC comprising geminivirus CI or AC1 wild-type or mutant sequences that
 CC negatively interfere in trans with geminiviral replication during
 CC infection. Such transgenic plants are resistant to viral infection. The
 CC AC1/CI genes are especially from BGWV, tomato mottle virus or tomato
 CC yellow leaf curl virus (see AAT9282-93) and encode polypeptides (see
 CC AAM34324-35) that have mutations in the highly conserved DNA-nicking
 CC and/or the NTP-binding domains. (Updated on 17-OCT-2003 to standardise OS
 CC field)
 CC
 XX
 SQ Sequence 1183 BP; 371 A; 277 C; 249 G; 286 T; 0 U; 0 Other;
 Query Match 64.1%; Score 694.6; DB 2; Length 1183;
 Best Local Similarity 77.8%; Pred. No. 4.3e-210;
 Matches 838; Conservative 0; Mismatches 239; Indels 0; Gaps 0;

QY 1 ATGCCCCACCAAGAAATTTAGAGTCAAGTCAAGAACTATTCTTCACTTATCCCCAG 60
 DB 1 ATGCAACCACTCAAGATTTAGAGTCAAGTCAAGAACTATTCTTCACTTATCCCCAG 60
 QY 61 TGGCTCTATCTAAGAAAGACCTTCCCAATTACAAAACCTAAATACCCAGTCAAC 120
 DB 61 TGGCCCTATACCGAAGAAAGATTTCTTCCCACTTCAAGAAATTCAGCCAGCAAT 120
 QY 121 AAGAAATTCATCAAAATTTGAGAGAGCTTCATGAAATAGGGAGACCTCATCTCCATGTG 180
 DB 121 AAAAAATTCATCAAAAGTCTGAGAGAGCTTCATGAAATAGGGAGACCTCATCTTCATGCG 180
 QY 181 CTTGTCAGTTCGAAAGTAATGCAATGCAAGTAATCAAGATTTCTGACCTGGTCC 240
 DB 181 CTTATTCATTCGAAAGTAATGCTGTGCAAAATTAAGATTTCTGACCTGGTATCC 240
 QY 241 CCAACCCGGTCAAGCACTTTCCATCCGAATTTAGAGAGCTTAATGAGCTCCGACGTC 300
 DB 241 TCAACCGGTCAAGCACTTTCCATCCGAATTTAGAGAGCTTAATGAGCTCCGACGTC 300
 QY 301 AAATCATATCAGCAAGAGACGAGATCAATGCAATGAGGAGATTTCCAAATGACGGC 360
 DB 301 AAGGCATATCAGCAAGAGATGAGTCAATGCAATGAGGAGCAATTCAGATGACGGC 360
 QY 361 AGATCTGCAAGAGAGGCGACAGCTGCTAATGATTCATATGCGAAAGCAATTAATGCA 420
 DB 361 AGATCTGCAAGAGAGGCTGACAGCTGCTCAACGACTCATATGCAAGGCAATTAAGCA 420
 QY 421 GGTTCGGTCAATGCTGCTTAAGCGTTCTAAGGGAAGAACCAAAAGATTTGTATTA 480
 DB 421 GATTCAATTAATGCTGCTTGAACAATATGAAAGAAACCAACCGAAAGATTTAGTCTT 480
 QY 481 CAAATCATATCAATCGGCTTAACCTTAAGAAAGCAATTTCCGAAAGGCTCCGGAACGGTGG 540
 DB 481 CAACATACAAATCGGCTTCTAATCTGAAAGCAATTTCTTCTCAAGTCCGGAACCAATGG 540
 QY 541 GTTCTCATATTCAGGCTCTCTTTCTTCACTAAGCTTCTGACGAGATGAGATGGCG 600
 DB 541 GTTCTCATATTCGCTGCTGATCATTCGGAATGTTCCGGTGTATGCAAGATGGGTT 600
 QY 601 GATTAATTAATTCGGAAGGCTGACGCTGCCCGCCGGAATGACTGTAATGATATGTC 660
 DB 601 GACGACTAATTCGGAAGGCTTCCGCTGCGCGCGCGGAAGAAAGCACTAATTAATCATGTC 660

QY 661 GAGGTGATTCAGAAACAGGGAAGACGATGTGGGCGGTGCTTAAGGCCACATACTAT 720
 DB 661 GAAGGTGATTCAGAAACAGGGAAGACGATGTGGGCGGTGCTTAAGGCCACATACTAT 720
 QY 721 CTCAGTGAACCTAGACCTTCAATGTGCGAGTCTTCTGATGATGTCAGTAAAGTTC 780
 DB 721 TTGAGCGGTATTTGACCTTAATTCACGTGCTATTCGAACGACGATGAATCAACGTC 780
 QY 781 ATTGATGACATCGCACCGCATTTATCTAAGCTAAAGACCTGAAAGAAATGCTGGGGCC 840
 DB 781 ATTGATGACATTAAGCCCAATTTATTTGAATTAAGACCTGAAAGAAATTAATGGGCA 840
 QY 841 CAGAAATTTGGCAATCAATTAAGTACGATGAGTCAAGTCAATTAATTAAGCGCAATC 900
 DB 841 CAAAGGACTCGCAATTAATCTGAATTAATGAAAGCCGTTCAATTAAGGAGAAATA 900
 QY 901 CCAACATCGTGTCTTTCATCTGTGAGGGTCCAGCTAATAAGAGTTCTTAAGACAA 960
 DB 901 CCAATCATGCTGTGTGCAATTCAGGTGAGGGTCCAGTTAATAAGACTTCTGACAAA 960
 QY 961 GCGAATAATCAGGCTCAAGAACTGACCTATCAAGAAATGCGATCTTCATCACCCTACA 1020
 DB 961 GAAGAAACCGAGCTTTCACAACTGACCTATTCATTAATGCAATCTTCGTCACCTACA 1020
 QY 1021 GCCCCCTTATCAAGAGACACAGGCAAGCAAGAAACGGGCAATCAGAAAGCG 1077
 DB 1021 GCCCCCTTATCAAGACACACAGGATTCGCAACGTAAGCCATTCGTGAGCG 1077

RESULT 13
 AAA94701
 ID AAA94701 standard; DNA; 1651 BP.
 XX
 AC AAA94701;
 XX
 DT 15-JAN-2001 (first entry)
 XX
 DE pTrepN nucleotide sequence.
 XX
 KM Geminivirus; DNA-A; geminivirus replication inhibition; ac3 gene;
 KM transgenic plant; antiviral; gene therapy; bean golden mosaic virus;
 KM BGWV; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CaMV; ds.
 OS Bean golden mosaic virus.
 OS Cauliflower mosaic virus.
 OS Alfalfa mosaic virus.
 OS Synthetic.
 XX
 PN US6118048-A.
 XX
 PD 12-SEP-2000.
 XX
 PF 24-APR-1998; 98US-0006599.
 XX
 PR 25-APR-1997; 97US-0044925P.
 XX
 PA (MISC) WISCONSIN ALUMNI RES FOUND.
 XX
 PI Maxwell DP, Hanson SF;
 XX
 DR WPI; 2000-610861/58.
 XX
 PT Genetic construct comprising a mutant geminiviral rep gene, useful for
 PT producing a plant resistant to geminiviral infection.
 XX
 PS Example; Col 17-18; 14pp; English.
 XX
 CC The present sequence is pTrepN, a vector containing a CamV-35S promoter-
 CC driven rep gene derived from bean golden mosaic virus (BGWV)-GA. Site-
 CC directed mutagenesis was used to engineer an NcoI site in the start codon
 CC of the rep gene to facilitate cloning of DNA-nicking domain mutants. The
 CC resulting genetic constructs act as trans-dominant inhibitors of

geminiviral replication. When expressed in a plant cell, these inhibitors are able to dramatically reduce replication of geminiviruses. Genetic constructs that include sequences containing a portion of the ac3 gene in addition to the trans-dominant inhibitor exhibit increased efficiency and broadened specificity of inhibition of geminiviral replication. CC Geminiviruses are one of the greatest constraints on production of CC important crops, including cassava, beans, cowpeas, peppers, tomatoes and CC cotton. The effects of the virus can be overcome by using the genetic CC construct

SQ Sequence 1651 BP; 517 A; 392 C; 343 G; 399 T; 0 U; 0 Other;

Query Match Similarity:	64.1%;	Score 694.6;	DB3	Length 1651;
Best Local Similarity:	77.8%;	Pred. No. 5.1e-210;		
Matches 838;	Conservative	0;	Mismatches 239;	Indels 0; Gaps 0

QY	1	ATGCCCCACAAAGAAATTTAGAGTTGACATCAAGAACTAATTTCTTAATTAATCCGAG	60
Db	469	ATGGCACCACTCCAAAGATTTTAGAGTTGAGTCGAAAACTAATTTCTCACTTAATCTCGT	528
QY	61	TGCTCTATCTTAAAGAAAGCATTTTCCCAATTAACAACCTTAATATCCCACTCAAC	120
Db	529	TGCCCTTAATCCGAAAGAAAGATTTCTTTGCAACTTCAGAAATTAACAAGCCACGAAT	588
QY	121	AAGAAATTCATCAAAATTTGCAAGAGCTTCATGAAATATGGGGAACCTCATCTCATATG	180
Db	589	AAAAATTCATCAAGTCTGTGAGGAAGTCACGGAATATGGAACTCATATTTCAATGCG	648
QY	181	CTGTGTCAGTTGCAAGGTAGTACCAATGACGAATTAACAGATTTCTTGACCTGTGTTCC	240
Db	649	CTTATTCAAATTCGAAAGTAAATTTGCTGTGCACAATTAATAAGATTTGTCGACTGGATCC	708
QY	241	CCAAACCGGTCAGACATTTTCCATTCGGAATATTCAGGGAGCTTAATTCGAGTCCGACGTC	300
Db	709	TCAACCAAGGTAGCACTTTTCCATTCGAACTATTCAGGAGGCTTAATTCAAAGTTCACAAGCTC	768
QY	301	AAATCATATCATCGACAGAGGAGGAGATCAATCGAATGGAGGAGATTTCCAAATTCGACGAC	360
Db	769	AAGCATATCATTCGACAAAGATGAGTCAATTCGAATGGGACAAATTCGAAGTCCAGCGC	828
QY	361	AGATCTGCGAAGGAGGCGCAGACGTTCTGTCTAATGATTCATATGCGAAAGCATTAATATGCA	420
Db	829	AGATCTGCAAGAGGAGGTACAGAGCTCTGCAACGACTCATATGCAAGGCAATTAACGCA	888
QY	421	GCTTCGCTTCATCTGCTCTTAGCGGTTCTAAGGAAAGAACCCAAAAGATTTTGATATTA	480
Db	889	GATTCAAATTTGAATCTGCTCTTGAACAATATTTGAAGGAAGAACCCAAAAGATTAATCTCTT	948
QY	481	CAAAATCATTAACATCCGCTCTTAACCTTAAGCGAATATTCGAAAGGCTCCGGAACCGTGG	540
Db	949	CAACATCAACATATCCGTTCTTAATTCGAAACGGAATCTTGTCAAAAGTGCAGAACCATATG	1008
QY	541	GTTCCCTCAATTCGAAGTCTCTTCTTTCACTAAGTTTCTGACGAGATGACGAATGGGCG	600
Db	1009	GTTCCCTCAATTTCCGTTGTCATCAATTCATCAATGTTCCGGTGTATGCAAGAAATGGGTT	1068
QY	601	GATTAATTAATTCGGGAGCGGTGAGCGCTGCGCGCGCGGATAGACCTGTAAGTATCATCTGC	660
Db	1069	GACGACTAATTTTCGGAAGGGGTTCCGCTGCGCGCGCGGAAAGACTTAATTAATGATCATCTGC	1128
QY	661	GAGGAGTATTCAGAAACAGGAGAAAGCATATGTGGGCGCGTGCCTTAGGCGCCACATTAATAT	720
Db	1129	GAAAGTGAATTCACGAAACCGGAAAGCAATATGTGGGCTCGTGCACTTAGACACATTAATAT	1188
QY	721	CTCAGTGAACACTTGAATTTCAATGATGGAATCTTCTCGAATGATGTGCAATTAACGTC	780
Db	1189	TTGAGCGGTCAATTTGGACTTTAATTCACGTGTCTTAATTCMAAGCAGTGGAAATTAACAAGTC	1248
QY	781	ATTATGATCATCGCAACCGCATTAATCTTAAGCTTAAGCACTGGAAAGAAATGCTGGGGGCG	840
Db	1249	ATTATGATCATTAAGCCCAATTAATTTGAAGTTAAAGCACTGGAAAGAACTAATTTGGGGCA	1308
QY	841	CAGAAAGATTGGCAATCAAAATTCGAAGTACGATTAAGCAAGTTCAAATTAAGGCGGAATC	900

Db 1309 CAAAGGACTGGCAATCTTAATCTGTAATATGGAAGCCGGTTCAAAATTAAAGAGGATA 1368

Qy 901 CCAGCAATCGTGCTTTGCAAATCTGTGTAGGGTGCCAGTATAAAGATTCTTAGACAAA 960

Db 1369 CCATCATCTCGTGTGTGCATCTCAGGTGAGGGTTCCAGTTATAAAGACTTCTGTGACAAA 1428

Qy 961 GCAGAAAAATACAGGTCTCAAGAACTGSACTATCAAGAATCCGATCTTCAATACCCTTACA 1020

Db 1429 GAAAGAAAACGAGTTTACCACTGSACTATTCATATGCGATCTTCTGTACCCCTTACA 1488

Qy 1021 GCCCCCTCTATATCAAGAGACACAAGGCAAGCCCAAGAAAACGGCAATTCAGAMGGCG 1077

Db 1489 GCCCCCTCTATATCAAGAGACACAAGGATTTGCCAAACGTAGAGCCATTTGCTGACG 1545

RESULT 14
AAT93291
ID AAT93291 standard; DNA; 1062 BP
VY

AC	AAT93291;
XX	
DT	17-OCT-2003 (revised)
DT	27-APR-1998 (first entry)
XX	
XX	
DE	Bean golden mosaic geminivirus C1 mutant ORF BGAC221.
XX	
KW	Geminivirus; BGMV; C1 gene; transdominant mutation; transgenic plant;
KX	disease resistance; ss; cyclic; circular.
XX	
OS	Bean golden mosaic virus; type II isolate Guatemala.
XX	
PN	MO939110-A1.
PD	
XX	23-OCT-1997.
PF	
XX	15-APR-1997; 97WO-US006300.
PR	
XX	16-APR-1996; 96US-0015517P.
PA	(SEMT-) SEMINIS VEGETABLE SEEDS INC.
XX	(WISC) WISCONSIN ALUMNI RES FOUND.
P1	
XX	Stout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;
DR	
XX	WPI: 1997-526447/48.
DR	P-PADB; AAM34333.
XX	
PT	Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
PT	genes - have increased resistance to geminivirus infection e.g. tomato
PT	mottle virus, tomato yellow leaf curl virus or bean golden mosaic
PT	geminivirus.
PS	
XX	
XX	Claim 13; Page 107-109; 132PP; English.
CC	This DNA sequence comprises construct BGAC221 that codes for a
CC	transdominant lethal mutant (see AAM34333) of the CI protein (see
CC	AAM34338) of bean golden mosaic virus (BGMV). It was obtained by Kunkel
CC	mutagenesis of the wild-type CI gene (see AAT93314). CI is required for
CC	replicating. The invention involves production of transgenic plants
CC	containing DNA comprising geminivirus CI or AC1 wild-type or mutant
CC	sequences that negatively interfere in trans with geminiviral replicatio
CC	during infection. Such transgenic plants are resistant to viral
CC	infection. The AC1/CI genes are especially from BGMV, tomato mottle viru
CC	or tomato yellow leaf curl virus (see AAT93282-93) and encode
CC	polypeptides (see AAM34324-35) that have mutations in the highly
CC	conserved DNA-nicking and/or the NTP-binding domains. (Updated on 17-OCT
CC	2003 to standardise OS field)
XX	
SQ	Sequence 1062 BP; 339 A; 245 C; 219 G; 259 T; 0 U; 0 Other;
Query Match	63.8%; Score 691.2; DB 2; Length 1062;
Best Local Similarity	78.4%; Pfd. No. 4.9e-209;

Matches 828; Conservative 0; Mismatches 228; Indels 0; Gaps 0;

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QY 1 ATGCCCCACCAAGAAATTTAGAGTTCAAGTCAAGAACTATTTCTTACTTATCCAG 60
DB 1 ATGCCACACCTCAAAAGATTAGAGTTCAGTCGAAAACTATTTCTTCACTTATCTCTGT 60
QY 61 TGGCTCTATCTAAAGAAAGACATTTCCCAATTTACAAAACCTAAATACCAGTCAC 120
DB 61 TGGCTCTATCTAAAGAAAGAGTTCTTTCCGACTTCGAAAGATTCATACAGCCACGAT 120
QY 121 AAGAAATTCACAAATTTGACAGAGCTTCATGAAAAATGGGAGCTCATCTTCATGTG 180
DB 121 AAAAAATTCACAAAGTCTGTGAGGAACGTCAACGATGGTGAACCTCATCTTCATGCG 180
QY 181 CTGTTCAGTTCCGAAGGTAAATACCAATGCACGAATACAGATTTCTTCAGCTGTCTCC 240
DB 181 CTATATTAATTCGAAGGTAAATGTGTCTGACAAATTAAGATTTGACCTGTGTATCC 240
QY 241 CCAACCCGGTCAGACATTTTCATCCGAAATATTCAGGAGCTAAATCGAGCTCCGAGTC 300
DB 241 TCAACCAAGTCAGACCTTTTCATCCGAACTTCAGGAGCTAAATCAAGTTCAGAGTC 300
QY 301 AAATCATATACGACGACGAGATGAGATCAATCGAATGGGAGATTTCCAAATGACGCG 360
DB 301 AAGGCATATACGACGACGAGATGAGATCAATCGAATGGGAGCAATTCGAAATGACGCG 360
QY 361 AGATTCGCCAGAGAGCCGACGACTCTGCTAATATTCATATGCGAAAGCTTAAATGCA 420
DB 361 AGATCTGCAAGAGAGGTGACGAGCTGCGCAACGATCATATGCAAGGCAATTAAGCA 420
QY 421 GGTTCGGTCAATCTGCTTACGCGTCTAAGGGGAAACCAACAAAGATTTGTATTA 480
DB 421 GATTCAATGATTTGCTTACAAATATGAGAGAAACACGGAAGATTTAGTCTT 480
QY 481 CAAAATCATACATCCGCTCTAACCCTAGAACGAATTTCCGAAGGCTCCGGAACGCTGG 540
DB 481 CAACATCAACAACCCGTTCTAATCTCGAACGATCTTCGCAAGTGCGGGAACCATGG 540
QY 541 GTTCCTCATATTCAGTCTCTTCTTCACTAAGCTTCTGACGAGATGGGAGATGGCG 600
DB 541 GTTCCTCATATTCGTTGTCAATCAATCAATTTCCGTTGTATGCAAGATGGAGT 600
QY 601 GATATATTTTCCGAGCGAGTGAAGCTGCGCGCGGATAGACCTGTAAGTATCATGTC 660
DB 601 GAGGACATTTCCGAAAGGGGTCCGCTGCGCGCGGGAAGAACTTATTAAGTATCATGTC 660
QY 661 GAGGTGATTCAGAACAGGAGACGATGTGGCGGTGGCTTGGAGCCCACTAATCTAT 720
DB 661 AGAGGTGATTCAGAACCGGAAAGACATGTGGGCTGTGCAATTAAGACCATATTAAT 720
QY 721 CTGAGTGAGACCTAGACTTCAATGTCGAGTCTTCTGAAATGTCAGTATTAAGCTC 780
DB 721 TTGAGCGGTCAATTTGACTTAAATTCAGTGTCTATTCGAACGAGTGGAATCAACGTC 780
QY 781 ATTGATGACATCCGACCGCATTTATCTAAGCTTAAAGACTGGAAGAAATGCTGGGCGC 840
DB 781 ATTGATGACATTAAGCCCAATTTATTAAGTAAAGACTGGAAGAAATTAATGGGCGA 840
QY 841 CAGAAAGATTGGCAATCAAAATGCAAGTACGTAAGCCAGTTCAAATTAAGGCGGAATC 900
DB 841 CAAAGAGACTGGCAATCTAATCTGTAATATGGAAGGCGGTTCAAAATTAAGGAGATA 900
QY 901 CCAAGCATGTCGCTTTCATCTGTCGTCGAGGTCGAGCTTAAGAAGTCTTGAACAA 960
DB 901 CCAATCAATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 960
QY 961 GCAGAAATTAAGGTCCTCAAGAACTGATCAATCAAGATGAGATCTTCATCACTCCACA 1020
DB 961 GAGAAATTAAGGTCCTCAAGAACTGATCAATCAAGATGAGATCTTCATCACTCCACA 1020
QY 1021 GCCCCTCTATCAAGAGACACAGGCAAGCCAA 1056
DB 1021 GCCCCTCTATCAAGAGACACAGGATGGCCAA 1056

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RESULT 15
AAT93292
ID AAT93292 standard; DNA; 1062 BP.
XX
AC AAT93292;
XX
DT 17-OCT-2003 (revised)
DT 27-APR-1998 (first entry)
XX
DE Bean golden mosaic geminivirus CI mutant ORF BGAC228.
XX
KW Geminivirus; BGWV; CI gene; transdominant mutation; transgenic plant;
KW disease resistance; ser; cyclic; circular.
XX
OS Bean golden mosaic virus; type II isolate Guatemala.
XX
PN W09739110-A1.
XX
PD 23-OCT-1997.
XX
PF 15-APR-1997; 97WO-US006300.
XX
PR 16-APR-1996; 96US-001551P.
XX
PA (SEMT-) SEMINIS VEGETABLE SEEDS INC.
PA (WISC) WISCONSIN ALUMNI RES FOUND.
XX
PI Scout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;
XX
XX WPI: 1997-526447/48.
DR P-PSDB; AAM34334.
XX
PT Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
PT genes - have increased resistance to geminivirus infection e.g. tomato
PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic
PT geminivirus.
XX
PS Claim 13; Page 111-112; 132pp; English.
XX
CC This DNA sequence comprises construct BGAC228 that codes for a
CC transdominant lethal mutant (see AAM34334) of the CI protein (see
CC AAM34338) of bean golden mosaic virus (BGWV). It was obtained by Kunze
CC mutagenesis of the wild-type CI gene (see AAT93314). CI is required for
CC replication. The invention involves production of transgenic plants
CC containing DNA comprising geminivirus CI or AC1 wild-type or mutant
CC sequences that negatively interfere in trans with geminiviral replication
CC during infection. Such transgenic plants are resistant to viral
CC infection. The AC1/CI genes are especially from BGWV, tomato mottle virus
CC or tomato yellow leaf curl virus (see AAT93282-93) and encode
CC polypeptides (see AAM34324-35) that have mutations in the highly
CC conserved DNA-nicking and/or the NTP-binding domains. (Updated on 17-OCT-
CC 2003 to standardise OS field)
XX
SO Sequence 1062 BP; 338 A; 247 C; 218 G; 259 T; 0 U; 0 Other;

Query Match 53.8%; Score 691.2; DB 2; Length 1062;
Best Local Similarity 78.4%; Pred. No. 4.9e-209;
Matches 828; Conservative 0; Mismatches 228; Indels 0; Gaps 0;

```

QY 1 ATGCCCCACCAAGAAATTTAGAGTTCAAGTCAAGAACTATTTCTTACTTATCCAG 60
DB 1 ATGCCACACCTCAAAAGATTAGAGTTCAGTCGAAAACTATTTCTTCACTTATCTCTGT 60
QY 61 TGGCTCTATCTAAAGAAAGACATTTCCCAATTTACAAAACCTAAATACCAGTCAC 120
DB 61 TGGCTCTATCTAAAGAAAGAGTTCTTTCCGACTTCGAAAGATTCATACAGCCACGAT 120
QY 121 AAGAAATTCACAAATTTGACAGAGCTTCATGAAAAATGGGAGCTCATCTTCATGTG 180
DB 121 AAAAAATTCACAAAGTCTGTGAGGAACGTCAACGATGGTGAACCTCATCTTCATGCG 180
QY 181 CTGTTCAGTTCCGAAGGTAAATACCAATGCACGAATACAGATTTCTTCAGCTGTCTCC 240
DB 181 CTATATTAATTCGAAGGTAAATGTGTCTGACAAATTAAGATTTGACCTGTGTATCC 240
QY 241 CCAACCCGGTCAGACATTTTCATCCGAAATATTCAGGAGCTAAATCGAGCTCCGAGTC 300
DB 241 TCAACCAAGTCAGACCTTTTCATCCGAACTTCAGGAGCTAAATCAAGTTCAGAGTC 300
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DB 301 AAGGCATATACGACGACGAGATGAGATCAATCGAATGGGAGCAATTCGAAATGACGCG 360
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DB 361 AGATCTGCAAGAGAGGTGACGAGCTGCGCAACGATCATATGCAAGGCAATTAAGCA 420
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QY 481 CAAAATCATACATCCGCTCTAACCCTAGAACGAATTTCCGAAGGCTCCGGAACGCTGG 540
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QY 541 GTTCCTCATATTCAGTCTCTTCTTCACTAAGCTTCTGACGAGATGGGAGATGGCG 600
DB 541 GTTCCTCATATTCGTTGTCAATCAATCAATTTCCGTTGTATGCAAGATGGAGT 600
QY 601 GATATATTTTCCGAGCGAGTGAAGCTGCGCGCGGATAGACCTGTAAGTATCATGTC 660
DB 601 GAGGACATTTCCGAAAGGGGTCCGCTGCGCGCGGGAAGAACTTATTAAGTATCATGTC 660
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DB 1021 GCCCCCTCTATCAAGACACACAGATTCCAA 1056

Search completed: December 4, 2004, 13:50:53
Job time : 608 secs

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OM nucleic - nucleic search, using sw model

Run on: December 4, 2004, 13:17:10 ; Search time 116 Seconds

(without alignments)
6636.072 Million cell updates/sec

Title: US-09-491-063A-1

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Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1047.8	96.7	1162	3	US-08-838-151A-1 Sequence 1, Appl
2	1044.6	96.5	1169	3	US-08-838-151A-5 Sequence 5, Appl
3	1043	96.3	1169	3	US-08-838-151A-7 Sequence 7, Appl
4	1040.8	96.1	1262	3	US-08-838-151A-17 Sequence 17, Appl
5	1039.8	96.0	1169	3	US-08-838-151A-3 Sequence 3, Appl
6	1033.8	95.5	1166	3	US-08-838-151A-13 Sequence 13, Appl
7	702.2	64.8	1246	3	US-08-838-151A-15 Sequence 15, Appl
8	696.2	64.3	1183	3	US-08-838-151A-43 Sequence 43, Appl
9	696.2	64.3	1651	3	US-09-065-999-5 Sequence 5, Appl
10	696.2	64.3	1894	3	US-09-065-999-8 Sequence 8, Appl
11	696.2	64.3	2072	3	US-09-065-999-7 Sequence 7, Appl
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13	694.6	64.1	1651	3	US-09-065-999-6 Sequence 6, Appl
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15	691.2	63.8	1062	3	US-08-838-151A-51 Sequence 51, Appl
16	689.6	63.7	1062	3	US-08-838-151A-54 Sequence 54, Appl
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18	494.4	45.7	1145	3	US-08-809-1038-7 Sequence 7, Appl
19	492.8	45.5	1150	3	US-08-809-1038-3 Sequence 3, Appl
20	492.8	45.5	1150	3	US-08-809-1038-5 Sequence 5, Appl
21	479.4	44.3	1145	3	US-08-838-151A-19 Sequence 19, Appl
22	479.4	44.3	1145	3	US-08-838-151A-23 Sequence 23, Appl
23	479.4	44.3	1145	3	US-08-838-151A-26 Sequence 26, Appl
24	477.8	44.1	1145	3	US-08-838-151A-29 Sequence 29, Appl
25	418.4	38.6	1403	3	US-08-838-151A-59 Sequence 59, Appl
26	246.6	22.8	1403	3	US-08-838-151A-60 Sequence 60, Appl
27	185.2	17.1	780	3	US-08-838-151A-61 Sequence 61, Appl

28	47.2	4.4	517	4	US-09-936-552A-2 Sequence 2, Appl
29	45.8	4.2	1024	3	US-09-414-276-5 Sequence 5, Appl
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33	36.8	3.4	10236	3	US-09-453-7028-240 Sequence 240, App
34	34.2	3.2	784	2	US-08-750-654-1 Sequence 1, Appl
35	34.2	3.2	1141	4	US-09-806-708B-22 Sequence 22, Appl
36	34	3.1	3030	4	US-09-693-146-3 Sequence 3, Appl
37	33.6	3.1	832	4	US-09-621-976-2813 Sequence 2813, Ap
38	33.6	3.1	6268	4	US-09-566-921-57 Sequence 57, Appl
39	33.6	3.1	74962	4	US-09-685-853A-3 Sequence 3, Appl
40	33.4	3.1	389	4	US-09-621-976-8976 Sequence 8976, Ap
41	32.8	3.0	474	4	US-09-621-976-18033 Sequence 18033, A
42	32.8	3.0	1141	4	US-09-806-708B-22 Sequence 22, Appl
43	32.8	3.0	6407	2	US-08-616-844-7 Sequence 7, Appl
44	32.8	3.0	6407	2	US-08-599-654-7 Sequence 7, Appl
45	32.8	3.0	6407	3	US-08-944-868A-7 Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-838-151A-1
Sequence 1, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlgvist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiiviruses
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS: 63
ADDRESSER: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Gemini Virus
INDIVIDUAL ISOLATE: Florida
FEATURE:
NAME/KEY: CDS

LOCATION: 44..1127
PUBLICATION INFORMATION:
AUTHORS: Gilbertson, RL
AUTHORS: Hidayat, SH
AUTHORS: Papiomatias, EJ
AUTHORS: Rojas, MR
AUTHORS: Hou, YM
AUTHORS: Maxwell, DP
TITLE: Pseudorecombination between the infectious
TITLE: cloned DNA components of tomato mottle and bean
TITLE: dwarf mosaic geminiviruses.
JOURNAL: Jour. General Virol.
VOLUME: 74
PAGES: 23-31
DATE: 1993
US-08-838-151A-1

Query Match 96.7%; Score 1047.8; DB 3; Length 1162;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1061; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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QY 841 CAGAAAGATTGGCAATCAAAATTCGAAAGTGAAGGCACTTCAATTAAGGCGAATC 900
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QY 1081 GGT 1083
DB 1124 GGT 1126

RESULT 2

US-08-838-151A-5
Sequence 5, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1169 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Geminivirus
STRAIN: Florida

FEATURE:
NAME/KEY: CDS
LOCATION: 44.1127
US-08-838-151A-5

Query Match
Best Local Similarity 97.8%; Score 1044.6; DB 3; Length 1169;
Matches 1059; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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DB 584 GTTCTCTCAATTCAGATCTCTTCTTCACTAAGTTCTGACGAGATGACGAGATGGGCG 643
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QY 1081 GGT 1083
DB 1124 GGT 1126

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RESULT 3
US-08-838-151A-7
; Sequence 7, Application US/08838151A
; Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Steut, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSER: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1169 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Gemini Virus
STRAIN: Florida
FEATURE:
NAME/KEY: CDS
LOCATION: 44.1127
US-08-838-151A-7
Query Match
Best Local Similarity 96.3%; Score 1043; DB 3; Length 1169;
Matches 1058; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 1 ATGCCCCCAAGAAATTTAGATTGCTCAAGAAAGATTTTCTTAATTCCTCCAG 60
DB 44 ATGCCCCCAAGAAATTTAGATTGCTCAAGAAAGATTTTCTTAATTCCTCCAG 103

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Db 164 AAGAAATTCATCAAAATTTGAGAGAGCTTCATGAAAATGGGGAACCTCATCTTCATGTG 223
QY 181 CTGTTCAGTTCCAGAGTAACTACCAATGCAAGAAATGACATTTCTGACCTGCTCC 240
Db 224 CTGTTCAGTTCCAGAGTAACTACCAATGCAAGAAATGACATTTCTGACCTGCTCC 283
QY 241 CCAACCCGTCAGACATTTCCATCCGATTAATTCAGGAGCTAATGAGCTCCGAGCTC 300
Db 284 CCAACCCGTCAGACATTTCCATCCGATTAATTCAGGAGCTAATGAGCTCCGAGCTC 343
QY 301 AAATCATATACGACAAAGAGAGAGATACATCGAATGGGAGATTTCCAAATGACGAGC 360
Db 344 AAATCATATACGACAAAGAGAGAGATACATCGAATGGGAGATTTCCAAATGACGAGC 403
QY 361 AGATCTCCAG 420
Db 404 AGATCTCCAG 463
QY 421 GGTTCGTTCAATCTGCTTACGCGTTCTAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 464 AGTTCGTTCAATCTGCTTACGCGTTCTAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 523
QY 481 CAAATCATATACGAGCTCTACCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 524 CAAATCATATACGAGCTCTACCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 583
QY 541 GTTTCCTCATATTCAGAGCTCTTCTTCACTAAGCTTCTTCAAGAGAGAGAGAGAGAG 600
Db 584 GTTTCCTCATATTCAGAGCTCTTCTTCACTAAGCTTCTTCAAGAGAGAGAGAGAGAG 643
QY 601 GATTAATTAATTTCCGAG 660
Db 644 GATTAATTAATTTCCGAG 703
QY 661 GAGGATGATTCAAG 720
Db 704 GAGGATGATTCAAG 763
QY 721 CTGAGTGAACCTAAGCTTCAATGTCAGAGCTTCTTCAAGAGAGAGAGAGAGAGAG 780
Db 764 CTGAGTGAACCTAAGCTTCAATGTCAGAGCTTCTTCAAGAGAGAGAGAGAGAGAG 823
QY 781 ATTGATGACATCGACAGGCTTATCTAAGCTAAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db 824 ATTGATGACATCGACAGGCTTATCTAAGCTAAGAGAGAGAGAGAGAGAGAGAGAGAG 883
QY 841 CAGAAAGATTGGCAATCAAAATGGCAAGTACGTAAGCAGTTCAAATTAAGAGAGAGATC 900
Db 884 CAGAAAGATTGGCAATCAAAATGGCAAGTACGTAAGCAGTTCAAATTAAGAGAGAGATC 943
QY 901 CCGAGCATCGTCTTTCGCAATCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db 944 CCGAGCATCGTCTTTCGCAATCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1003
QY 961 GCAGAAATATCAGGCTCAAGAACTGACTATCAAGATGAGATCTTCATCAACCTCACA 1020
Db 1004 GCAGAAATATCAGGCTCAAGAACTGACTATCAAGATGAGATCTTCATCAACCTCACA 1063
QY 1021 GCGCCCTCTATCAAG 1080
Db 1064 GCGCCCTCTATCAAG 1123
QY 1081 GGT 1083
Db 1124 GGT 1126

RESULT 4
US-08-838-151A-17/c
Sequence 17, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlgren, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2602 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Geminiivirus
STRAIN: Florida
US-08-838-151A-17
Query Match 96.1%; Score 1040.8; DB 3; Length 2602;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1054; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 8 CACCAAGAAATTTAGAGTTCAGTCAAGAACTAATTTCTAATCTATCCAGTCTCTC 67
Db 2602 CACCAAGAAATTTAGAGTTCAGTCAAGAACTAATTTCTAATCTATCCAGTCTCTC 2543
QY 68 TATCTAAG 127
Db 2542 TATCTAAG 2483
QY 128 TCATCAAAATTTGAGAGAGCTTCATGAAGATGGGAGAGCTTCATCTCATGTGCTTTC 187
Db 2482 TCATCAAAATTTGAGAGAGCTTCATGAAGATGGGAGAGCTTCATCTCATGTGCTTTC 2423
QY 188 AGTTGAG 247
Db 2422 AGTTGAG 2363
QY 248 GGTTCAG 307
Db 2362 GGTTCAG 2303

QY	308	ACATCGACAAAGACGAGATTCATTCGAATGGGAGATTTCCAAATCGACGGCAGATCTG	367
Db	2202	ACATCGACAAAGACGAGATTCATTCGAATGGGAGATTTCCAAATCGACGGCAGATCTG	2243
QY	368	CCAGAGGAGCGCAGCAGTCTGCTAATGATTCATATGCGAAAGCATTTAATGCAAGGTCGG	427
Db	2242	CCAGAGGAGCGCAGCAGTCTGCTAATGATTCATATGCGAAAGCATTTAATGCAAGTTCGG	2183
QY	428	TTCAATCTGCTTACCGGTTCTTAAGGGAAGAACCAACCAAAAGTTTTGTATTTACAAATC	487
Db	2182	TTCAATCTGCTTACCGGTTCTTAAGGGAAGAACCAACCAAAAGTTTTGTATTTACAAATC	2123
QY	488	ATTAACATCCGCTCTAACCTTAGAACGAATATTTGCGAAAGGCTCCGGAACCGTGGGTTCTC	547
Db	2122	ATTAACATCCGCTCTAACCTTAGAACGAATATTTGCGAAAGGCTCCGGAACCGTGGGTTCTC	2065
QY	548	CATTTCAAAGTCTCTTCTTCACTAACGTTCTCGTAGAGATGCAAGAAATGGCGGATAAT	607
Db	2062	CATTTCAAAGTCTCTTCTTCACTAACGTTCTCGTAGAGATGCAAGAAATGGCGGATAAT	2003
QY	608	ATTTTCGGGACGGGTGACGCTGCGCGCCGGATAGACTCTGTAAATCATCGTCCAGGGTG	667
Db	2002	ATTTTCGGGACGGGTGACGCTGCGCGCCGGATAGACTCTGTAAATCATCGTCCAGGGTG	1943
QY	668	ATTTCAGAAACGGGAAAGACGATGTGGGGGGGCTTGGGCCCATATACATATCCAGTG	727
Db	1942	ATTTCAGAAACGGGAAAGACGATGTGGGGGGGCTTGGGCCCATATACATATCCAGTG	1883
QY	728	GACACCTAGACTTCAATGATGTCAGAGTCTTCTCGAATGATGTCAGATATAACGTCAATGATG	787
Db	1882	GACACCTAGACTTCAATGATGTCAGAGTCTTCTCGAATGATGTCAGATATAACGTCAATGATG	1822
QY	788	ACATCGCACCGCATTTATTTAAAGCTAAAGCACTGGAAAGAAATGCTGGGGGCCGAAAG	847
Db	1822	ACATCGCACCGCATTTATTTAAAGCTAAAGCACTGGAAAGAAATGCTGGGGGCCGAAAG	1763
QY	848	ATTGGCAATCAAAATTGCAAGTACGGTAAACCAATTCAAAATTAAGGGCGGAATCCACAGAA	907
Db	1762	ATTGGCAATCAAAATTGCAAGTACGGTAAACCAATTCAAAATTAAGGGCGGAATCCACAGAA	1703
QY	908	TGCGTCTTTGCAATCTCGTAGGGGTGCACGCTAATAAGAGTTCTTACAAAGCAGAGAA	967
Db	1702	TGCGTCTTTGCAATCTCGTAGGGGTGCACGCTAATAAGAGTTCTTACAAAGCAGAGAA	1644
QY	968	ATPACAGGCTTCAAGAACTGACCTATCAAGAAATGCGATCTTCAATCAACCTCAACAGCCCCC	1027
Db	1642	ATPACAGGCTTCAAGAACTGACCTGATCAAGAAATGCGATCTTCAATCAACCTCAACAGCCCCC	1583
QY	1028	TCATATCAAGAGACACACAGGCAAGCCAAAGAAACGGGCAATCAAGAAAGCCGACAGGT	1083
Db	1582	TCATATCAAGAGACACACAGGCAAGCCAAAGAAACGGGCAATCAAGAAAGCCGACAGGT	1527

RESULT 5
US-08-838-151A-3

```

1  GENERAL INFORMATION:
2
3  APPLICANT:  Stout, John T
4
5  APPLICANT:  Luu, Hang T
6
7  APPLICANT:  Maxwell, Douglas
8
9  APPLICANT:  Alquist, Paul
10
11 APPLICANT:  Hanson, Steve
12
13 TITLE OF INVENTION:  Transgenic Plants Expressing Geminivirus
14
15 TITLE OF INVENTION:  Genes
16
17 NUMBER OF SEQUENCES:  63
18
19 CORRESPONDENCE ADDRESS:
20
21 ADDRESSEE:  Dreesler, Rocky, Milnamow & Katz
22
23 STREET:  Two Prudential Plaza, Suite 4700
24
25 CITY:  Chicago
26
27 STATE:  Illinois
28
29 COUNTRY:  U.S.A.

```

```

1 ZIP: 60601
2 COMPUTER READABLE FORM:
3 MEDIUM TYPE: Floppy disk
4 OPERATING SYSTEM: IBM PC compatible
5 SOFTWARE: PC-DOS/MS-DOS
6 CURRENT APPLICATION DATA: Patent Release #1.0, Version #1.30
7 APPLICATION NUMBER: US/08/838,151A
8 FILING DATE:
9 CLASSIFICATION: 800
10 ATTORNEY/AGENT INFORMATION:
11 NAME: Mueller, Lisa V
12 REGISTRATION NUMBER: 38,978
13 REFERENCE/DOCKET NUMBER: SVS3801P0260
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: 312-616-5400
16 TELEFAX: 312-616-5460
17 INFORMATION FOR SEQ ID NO: 3:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 1169 base pairs
20 TYPE: nucleic acid
21 STRANDEDNESS: single
22 TOPOLOGY: circular
23 MOLECULE TYPE: DNA (genomic)
24 HYPOTHEICAL: NO
25 ANTI-SENSE: NO
26 ORIGINAL SOURCE:
27 ORGANISM: Tomato Mottle Gemini Virus
28 STRAIN: Florida
29 FEATURE:
30 NAME/KEY: CDS
31 LOCATION: 44..1127
32 PUBLICATION INFORMATION:
33 AUTHORS: Gilbertson, RL et al.
34 TITLE: Pseudorecombination between the infectious
35 TITLE: cloned DNA components of tomato mottle and bean
36 JOURNAL: Journal of General Virology
37 VOLUME: 74
38 PAGES: 23-31
39 DATE: 1993
40 US-08-838-151A-3
41
42 Query Match 96.0%; Score 1039.8; DB 3; Length 1169;
43 Best Local Similarity 97.5%; Pred. No. 0;
44 Matches 1056; Conservative 0; Mismatches 27; Indels 0; Gaps 0
45
46 1 ATGCCCCCAAGAAATTAGAGTTCAGTCAAGAACTATTTCTTAATCTATCCGAG 60
47 44 ATGCCCCCAAGAAATTAGAGTTCAGTCAAGAACTATTTCTTAATCTATCCGAG 103
48
49 61 TGTCTCTATTAAGAAGACCTTCCCAATTACAAAACCTAATATCCCGACTCAAC 120
50
51 104 TGCCTCTTGTCTTAAGAAGACCTTCCCAATTACAAAACCTAATATCCCGACTCAAT 163
52
53 121 AAGAAATTCATCAAAATTTGAGAGAGCTTCATGAAATGGGGAAACCTCATCTCCATGNG 180
54
55 164 AAGAAATTCATCAAAATTTGAGAGAGCTTCATGAAATGGGGAAACCTCATCTCCATGNG 223
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57 181 CTGTGTCAGTTCGAAGGTAAAGTATCAATGACGAATTAACAGATTTCTTGACCTGGTCTCC 240
58
59 224 CTGTGTCAGTTCGAAGGTAAAGTATCAATGACGAATTAACAGATTTCTTGACCTGGTCTCC 283
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61 241 CCATCCCGGTGAGCATTTTCATCCCAATTTTCAAGGAAGTAAATGAGCTCCGACGTC 300
62
63 284 CCAACCCGGTGAACAATTTTCATCCCAATTTTCAAGGAAGTAAATGAGCTCCGACGTC 343
64
65 301 AAATCATATCATCGACCAAGACGAGATTAATCGAATGGGGAGATTTTCCAATCGACGGC 360
66
67 344 AAATCATATCATCGACCAAGACGAGATTAATCGAATGGGGAGATTTTCCAATCGACGGC 403
68
69 361 AGATCTGCGAGAGAGGCGCAGCACTTGTCTAATGATTCATATGGGAAAGCATTAATGCA 420

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Db	404	AGATCTGCAGAGGAGGCCAGACAGTCTGCTATATGATTCATATGCGAAAGCGTTAAATGCA	463
QY	421	GGTTCGGTTCAATCTGCCTTAGCCGTTCTTAAGGGAACAACCAAAAGATTTGTATTA	480
Db	464	AGTTCGGTTCAATCTGCCTTAGCCGTTCTTAAGGGAACAACCAAAAGATTTGTATTA	523
QY	481	CAAAATCATTAATCCGCTTACCTAGAACGAATATTCGAAAGGCTCCGGAAACCGTG	540
Db	524	CAAAATCATTAATCCGCTTACCTAGAACGAATATTCGAAAGGCTCCGGAAACCGTG	583
QY	541	GTTCCCTCAATTTCAAGTCTCTTCTTTCACTAAAGTTCCTGACGAGATCAGGAATGAGCG	600
Db	584	GTTCCCTCAATTTCAAGTCTCTTCTTTCACTAAAGTTCCTGACGAGATCAGGAATGAGCG	643
QY	601	GATAATTAATTTCCGGAGCGGCTGAGCGCTGCGCCGCGATPAGACTGTAAATCATCTGTC	660
Db	644	GATAATTAATTTCCGGAGCGGCTGAGCGCTGCGCCGCGAGAGAACCTGTAAATCATCTGTC	703
QY	661	GAGGCTGATTTCAAGAACAGGGAACAGATATGAGGCGCGTTAGGCGCCATPAACAT	720
Db	704	GAGGCTGATTTCAAGAACAGGGAACAGATATGAGGCGCGTTAGGCGCCATPAACAT	763
QY	721	CTCAGTGGACACCTAGACTTCAATATGCTGAGTCTTCTGAAATGATGCAGATPAACGTC	780
Db	764	CTCAGTGGACACCTAGACTTCAATATGCTGAGTCTTCTGAAATGATGCAGATPAACGTC	823
QY	781	ATTGATGACATCGACCCGACTTATCTAAAGCTTAAAGCTAGAAAGAAATTCCTGGGGCC	840
Db	824	ATTAAATATCATCGACCCGACTTATCTAAAGCTTAAAGCTAGAAAGAAATTCGTAAGGGCC	883
QY	841	CAGAAAGATTGGCAATCAAAATTGCAAGTACGGTAAAGCCAGTTCAAAATTAAAGCGGAATC	900
Db	884	CAGAAAGATTGGCAATCAAAATTGCAAGTACGGTAAAGCCAGTTCAAAATTAAAGCGCGAATC	943
QY	901	CCAGCAATCGTGCCTTGGCAATCTGCTAGAGGCTGCACGCTTAAAGAGTTCTTAGACAAA	960
Db	944	CCAGCAATCGTGCCTTGGCAATCTGCTAGAGGCTGCACGCTTAAAGAGTTCTTAGACAAA	1003
QY	961	GCAGAAAAATACAGGCTTCMAAGAACTGGAATCTCAAGAAATGGCATCTTCAACCTCCACA	1020
Db	1004	GCAGAAAAATACAGGCTTCMAAGAACTGGAATCTGGAAGAAATGGCATCTTCAACCTCCACA	1063
QY	1021	GGCCCCCTCTATCAAGAGAGCACACAGGCAAGCCAAAGAACGGGCAATCAGAGGCGCAG	1080
Db	1064	GGCCCCCTCTATCAAGAGAGCACACAGGCAAGCCAAAGAACGGGCAATCAGAGGCGCAG	1123
QY	1081	GGT 1083	
Db	1124	GGT 1126	

RESULT 6
 US-08-838-151A-13
 Sequence 13, Application US/08838151A
 Patent No. 6291743
 GENERAL INFORMATION:
 APPLICANT: Scout, John T
 APPLICANT: Lau, Hang T
 APPLICANT: Maxwell, Douglas
 APPLICANT: Ahlquist, Paul
 APPLICANT: Hanson, Steve
 TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 TITLE OF INVENTION: Genes
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Dreessler, Rocky, Milnamow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

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1  COMPUTER: IBM PC compatible
2  OPERATING SYSTEM: PC-DOS/MS-DOS
3  SOFTWARE: PatentIn Release #1.0, Version #1.30
4  CURRENT APPLICATION DATA:
5  APPLICATION NUMBER: US/08/938,151A
6  FILING DATE:
7  CLASSIFICATION: 800
8  ATTORNEY/AGENT INFORMATION:
9  NAME: Mueller, Lisa V
10 REGISTRATION NUMBER: 38,978
11 REFERENCE/DOCKET NUMBER: SVS3801P0260
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: 312-616-5400
14 TELEFAX: 312-616-5460
15 INFORMATION FOR SEQ ID NO: 13:
16 SEQUENCE CHARACTERISTICS:
17 LENGTH: 1166 base pairs
18 TYPE: nucleic acid
19 STRANDEDNESS: single
20 TOPOLOGY: circular
21 MOLECULE TYPE: DNA (genomic)
22 HYPOTHETICAL: NO
23 ANTI-SENSE: NO
24 ORIGINAL SOURCE:
25 ORGANISM: Tomato Mottle Geminivirus
26 INDIVIDUAL ISOLATE: Florida
27 FEATURE:
28 NAME/KEY: CDS
29 LOCATION: 44..436
30 US-08-838-151A-13

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Query Match	Similarity	Score	ID	Length
Best Local	97.6%	Pred. No. 0		
Matches 1061	Conservative	0	Mismatches 22	Indels 4
				Gaps 1
QY	1	ATGCCCCCAAAAGAAATTTAGAGTTCACTCAAGAACTATTTCTACTATCCCGAC	60	
DB	44	ATGCCCCCAAAAGAAATTTAGAGTTCACTCAAGAACTATTTCTACTATCCACAG	103	
QY	61	TGCTCTCTATTAAGAAGAGCACTTCCCAATTACAAACCTTAATACCCAGTCAAC	120	
DB	104	TGCTCTTGTCTAAGAAGAGCACTTCCCAATTACAAACCTTAATACCCAGTCAAT	163	
QY	121	AAGAAATTCATCAAAATTTGCAAGAGCTTCATGMAATTTGGGGAACCTCATCTCATGTG	180	
DB	164	AAGAAATTCATCAAAATTTGCAAGAGCTTCATGMAATTTGGGGAACCTCATCTCATGTG	223	
QY	181	CTTGTTCACTTCGAAGGTAAAGTAACTCAATGCAAGAACTAACATTTCTTGACCTGGTCTCC	240	
DB	224	CTTGTTCACTTCGAAGGTAAAGTAACTCAATGCAAGAACTAACATTTCTTGACCTGGTCTCC	283	
QY	241	CCAACCCCGGTGAGACATTTCCATCCGAATTTTCAGGAGGTAAATTCAGCTCCGACGTC	300	
DB	284	CCAACCCCGGTGAGACATTTCCATCCGAATTTTCAGGAGGTAAATTCAGCTCCGACGTC	343	
QY	301	AAATCATTCATCGACAAAGAGCGAGATTCATTCGAATGGGAGATTTTCCAAATCGACGGC	360	
DB	344	AAATCATTCATCGACAAAGAGCGAGATTCATTCGAATGGGAGATTTTCCAAATCGACGGC	403	
QY	361	A-----GATCTCCAGAGAGGCCGACAGCTGCTATATTCATTCAGAAAGCACTTAA	416	
DB	404	AGATCGATCTGCCAGAGAGGCCGACAGCTGCTATATTCATTCAGAAAGCGTTAA	463	
QY	417	TGCAGGTTCCGTTCAATTTGCTCTTAAGCGGTTCTAAGGGAAGAACCAACCAAAAGATTTTGT	476	
DB	464	TGCAGGTTCCGTTCAATTTGCTCTTAAGCGGTTCTAAGGGAAGAACCAACCAAAAGATTTTGT	523	
QY	477	ATTACAAATCATTAACATCCGCTCTAACCTTGAAGAGATTTTTCGAAAGGCTCCGGAAC	536	
DB	524	ATTACAAATCATTAACATCCGCTCTAACCTTGAAGAGATTTTTCGAAAGGCTCCGGAAC	583	
QY	537	GTGGGTTCTTCATTTCAAGTCTCTTCTTCACTAAGCTTCTGACGAGATCGAAGATG	596	

Db 584 GTGGGTTCCCTCCATTTCAAGTCTCTTCTTCACTAAGTTCGAGAGATGACGAATG 643
 QY 597 GCGGATTAATTTATTTGGGAGCGGAGTACGCTCGCGCGCGGATAGACCTGTAAATATCAT 656
 Db 644 GCGGATTAATTTATTTGGGAGCGGAGTACGCTCGCGCGCGGATAGACCTGTAAATATCAT 703
 QY 657 CGTGGAGGGGATTCAGAAACAGGAAAGAGATGTGGGCGCGGCTAGAGCCCACTAA 716
 Db 704 CGTGGAGGGGATTCAGAAACAGGAAAGAGATGTGGGCGCGGCTAGAGCCCACTAA 763
 QY 717 CTATCTCAGTGAACACCTAGACTTCAATGTGTGAGTCTTCTGCAATGATGAGATATA 776
 Db 764 CTATCTCAGTGAACACCTAGACTTCAATGTGTGAGTCTTCTGCAATGATGAGATATA 823
 QY 777 CGTCAATGATGACATGCGACCGCATTAATCTTAAAGCTAAAGCACTGGAAAGATTGCTGG 836
 Db 824 CGTCAATGATGACATGCGACCGCATTAATCTTAAAGCTAAAGCACTGGAAAGATTGCTAG 883
 QY 837 GCGCCGAAAGATTTGGCAATCAAAATTTGCAAGTACGGTAACCGCTTCAATTTAAAGCCG 896
 Db 884 GCGCCGAAAGATTTGGCAATCAAAATTTGCAAGTACGGTAACCGCTTCAATTTAAAGCCG 943
 QY 897 AATCCAGCAATGCTGCTTTCATCTCTGTGAGGGGTGCGAGCTATTAAGATTCTTGA 956
 Db 944 AATCCAGCAATGCTGCTTTCATCTCTGTGAGGGGTGCGAGCTATTAAGATTCTTGA 1003
 QY 957 CAAGAGAAATATACAGGTCTCAAGAACTGCACTATCAAGATGCGATCTTCAACCT 1016
 Db 1004 CAAGAGAAATATACAGGTCTTAAAGAACTGCACTATCAAGATGCGATCTTCAACCT 1063
 QY 1017 CAGAGCCCCCTTATCAAGAGACACACAGGCAAGCAAGGCAATCAAGAGC 1076
 Db 1064 CAGAGCCCCCTTATCAAGAGACACACAGGCAAGCAAGGCAATCAAGAGC 1123
 QY 1077 GCAGGCT 1083
 Db 1124 GCAGGCT 1130

RESULT 7
 US-08-838-151A-15
 ; Sequence 15, Application US/08838151A
 ; Patent No. 6291743
 ; GENERAL INFORMATION:
 ; APPLICANT: Stout, John T
 ; APPLICANT: Luu, Hang T
 ; APPLICANT: Maxwell, Douglas
 ; APPLICANT: Ahlquist, Paul
 ; APPLICANT: Hanson, Steve
 ; TITLE OF INVENTION: Transgenic Plants Expressing Gemminivirus
 ; NUMBER OF INVENTION: Genes
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 ; STREET: Two Prudential Plaza, Suite 4700
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: U.S.A.
 ; ZIP: 60601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/838,151A
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mueller, Lisa V
 ; REGISTRATION NUMBER: 38,978
 ; REFERENCE/DOCKET NUMBER: SVS3801P0260
 ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-616-5400
 ; TELEFAX: 312-616-5460
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1246 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Tomato Mottle Gemminivirus
 ; STRAIN: Florida
 ; PUBLICATION INFORMATION:
 ; AUTHORS: Gilbertson, RL
 ; AUTHORS: Hidayat, SH
 ; AUTHORS: Paplomatas, EJ
 ; AUTHORS: Rojas, MR
 ; AUTHORS: Hou, YW
 ; AUTHORS: Maxwell, DP
 ; TITLE: Pseudorecombination between the infectious
 ; TITLE: cloned DNA components of tomato mottle and bean
 ; TITLE: dwarf mosaic gemminiviruses.
 ; JOURNAL: Journal of General Virology
 ; VOLUME: 74
 ; PAGES: 23-31
 ; DATE: 1993
 ; US-08-838-151A-15

Query Match 64.8%; Score 702.2; DB 3; Length 1246;
 Best Local Similarity 98.2%; Pct. No. 1.4e-220;
 Matches 710; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 361 AGATCTGCCAGAGAGAGGAGCGAGCTGCTAATGATTCATATGCAAGCAATTAATGCA 420
 Db 1 AGATCTGCCAGAGAGAGGAGCGAGCTGCTAATGATTCATATGCAAGCAATTAATGCA 60
 QY 421 GGTTCGTTCAATCTGCTTTAGCGGTTCTAAGGAAACACCAAAAGATTTGTATTA 480
 Db 61 AGTTGCTTCAATCTGCTTTAGCGGTTCTAAGGAAACACCAAAAGATTTGTATTA 120
 QY 481 CAATATCATACATCCGCTCTAATCTAAGCAATTTGGCAAAAGCTCCGGAACCGTGG 540
 Db 121 CAATATCATACATCCGCTCTAATCTAAGCAATTTGGCAAAAGCTCCGGAACCGTGG 180
 QY 541 GTTCCTCAATTCATGCTCTTCTTCACTAAGCTCTGACGAGATGACGAGATGGGCG 600
 Db 181 GTTCCTCAATTCATGCTCTTCTTCACTAAGCTCTGACGAGATGACGAGATGGGCG 240
 QY 601 GATTAATTAATTTGGGAGCGGCTGACGCTGCGCGCGGATAGACCTGTAAATCATGTC 660
 Db 241 GATTAATTAATTTGGGAGCGGCTGACGCTGCGCGCGGATAGACCTGTAAATCATGTC 300
 QY 661 GAGGAGATTCAGAAACAGGAAAGAGATGTGGGCGCGGCTTAGGCCCACTAACTAT 720
 Db 301 GAGGAGATTCAGAAACAGGAAAGAGATGTGGGCGCGGCTTAGGCCCACTAACTAT 360
 QY 721 CTCAGTGAACCTAGACTTCAATGTGTGAGTCTTCTGCAATGATGAGTAAAGTGC 780
 Db 361 CTCAGTGAACCTAGACTTCAATGTGTGAGTCTTCTGCAATGATGAGTAAAGTGC 420
 QY 781 ATTGATGACATGCGACCGCATTAATCTTAAAGCTAAAGCACTGGAAGATTTGCGGGCC 840
 Db 421 ATTGATGACATGCGACCGCATTAATCTTAAAGCTAAAGCACTGGAAGATTTGCGGGCC 480
 QY 841 CAGAAAGATTTGGCAATCAAAATTTGCAAGTACCGTAACCGCTTCAATTTAAAGCCGGAATC 900
 Db 481 CAGAAAGATTTGGCAATCAAAATTTGCAAGTACCGTAACCGCTTCAATTTAAAGCCGGAATC 540
 QY 901 CCAGCAATGCTGCTTTCATCTCTGTGAGGGGTGCGAGCTATTAAGATTCTTGAAGCAAA 960
 Db 541 CCAGCAATGCTGCTTTCATCTCTGTGAGGGGTGCGAGCTATTAAGATTCTTGAAGCAAA 600

QY 961 GCAGAAATACAGCTCTCAAGACTGATCTATCAAGATGCTCTCATCACCCCTGACA 1020
 Db 601 GCAGAAATACAGCTCTCAAGACTGATCTCAAGATGCTCTCATCACCCCTGACA 660
 QY 1021 GCCCCCCCTTATCAAGAGACACAGGCAAGCCAGAAACGGGCAATCAGAAAGCCGAG 1080
 Db 661 GCCCCCCCTTATCAAGAGACACAGGCAAGCCAGAAACGGGCAATCAGAAAGCCGAG 720
 QY 1081 GGT 1083
 Db 721 GGT 723

RESULT 8
 US-08-838-151A-43
 ; Sequence 43, Application US/08838151A
 ; Patent No. 6291743
 ; GENERAL INFORMATION:
 ; APPLICANT: Stout, John T
 ; APPLICANT: Luu, Hang T
 ; APPLICANT: Maxwell, Douglas
 ; APPLICANT: Ahlquist, Paul
 ; APPLICANT: Hanson, Steve
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 ; TITLE OF INVENTION: Genes
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dressler, Rockey, Milamow & Katz
 ; STREET: Two Prudential Plaza, Suite 4700
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: U.S.A.
 ; ZIP: 60601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/838,151A
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mueller, Lisa V
 ; REGISTRATION NUMBER: 38,978
 ; REFERENCE/DOCKET NUMBER: SYS3801P0260
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-616-5400
 ; TELEFAX: 312-616-5460
 ; INFORMATION FOR SEQ ID NO: 43:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1183 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Bean Golden Mosaic Geminivirus
 ; STRAIN: Type II Isolates
 ; INDIVIDUAL ISOLATE: Guatemala
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..1059
 ; PUBLICATION INFORMATION:
 ; AUTHORS: Faria, JC
 ; AUTHORS: Gilbertson, RL
 ; AUTHORS: Hanson, SF
 ; AUTHORS: Morales, FJ
 ; AUTHORS: Ahlquist, P
 ; AUTHORS: Lomello, AO

AUTHORS: Maxwell, D
 ; TITLE: Bean Golden Mosaic Geminivirus Type II
 ; TITLE: Isolates from the Dominican Republic and
 ; TITLE: Guatemala: Nucleotide Sequences, Infectious
 ; TITLE: Pseudorecombinants, and Phylogenetic Relationships
 ; JOURNAL: Phytopathology
 ; VOLUME: 84
 ; ISSUE: 3
 ; PAGES: 321-329
 ; DATE: 1994
 ; US-08-838-151A-43

Query Match 64.3%; Score 696.2; DB 3; Length 1183;
 Best Local Similarity 77.9%; Pred. No. 1,3e-218;
 Matches 839; Conservative 0; Mismatches 238; Indels 0; Gaps 0;

QY 1 ATGCCCCCAACCAAGAAATTTAGAGTTCAAGAAAGATTTTCTTAATTCCTGAG 60
 Db 1 ATGCCCAACCTCAAGAAATTTAGAGTTCAAGAAAGATTTTCTTAATTCCTGAG 60
 QY 61 TGCTCTTATCTAAGAAAGAGACCTTCCCATTTACAAACCTAATACCCAGTCAAC 120
 Db 61 TGCTCTTATCTAAGAAAGAGACCTTCCCATTTACAAACCTAATACCCAGTCAAC 120
 QY 121 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAAATGGGAACTCATCTGATG 180
 Db 121 AAAAAATTCATCAAAAGTCTGTGAGAACTTCAGAAAGTGTGAACCTCATCTGATG 180
 QY 181 CTTGTCAGTTGGAAGTAATGCAATGACAGAAATACGATTTCTGACCTGCTCC 240
 Db 181 CTTATTCATCAAGAGTAATGCTGTCGCAAAATTAAGATTTGCTGACCTGCTCC 240
 QY 241 CCAACCCGTCACAGATTTCCATCCGAATTCAGGAGCTTAATGAGCTCCAGCTC 300
 Db 241 TCAACCAAGTCAGACCTTTCCATCCGAATTCAGGAGCTTAATGAGCTCCAGCTC 300
 QY 301 AAATCATATCATGACAAAGAGAGATACATGAAATGGGAGATTTCCAAATCGACGC 360
 Db 301 AAGGCATATCATGACAAAGAGATGAGATGACAAATGGGAGATTTCCAAATCGACGC 360
 QY 361 AGATCTGCCAGAGAGGCGACGCTGCTAATGATTCATATGCGAAAGCATTAATGCA 420
 Db 361 AGATCTGCCAGAGAGGCTGACGCTGCGCAAGACTCATATGCAAGCATTAATGCA 420
 QY 421 GGTTCGCTCAATCTGCTTAAGCGGCTTAAAGGAAAGAACCAAAAGATTTGATTA 480
 Db 421 GATTCATTAATTAATGCTGCTTAAGCAATTAATTAAGGAAAGAACCAAAAGATTTGATTA 480
 QY 481 CAATATCATATCATGCGCTTAACCTAAGACGATATTCGCAAGGCTCCGGAACCGTGG 540
 Db 481 CAATATCATATCATGCGCTTAAATCTGAAGGATTCGCTCAAAAGTCCGGAACCATGG 540
 QY 541 GTTCCTCATTTCAAGTCTCTTTCACTAAGCTTCGACGATGACGAGATGGGCG 600
 Db 541 GTTCCTCATTTCCGTTGATCATATCAATGATTCGCTGTTATGCAAGATGGGCTT 600
 QY 601 GATTAATTTTGGGAGCGGCTGACGCTGCGCGCGGATGACCTGATTAATCATATGCTC 660
 Db 601 GACGACTAATTTGGAAGGGGTTCCGCTGCGCGCGGAAAGACCTTAATTAATCATATGCTC 660
 QY 661 GAGGCTGATTCAGAAACAGGAAAGAGAGATGGGCGGCTGCTTAAGGCGGCAATATAT 720
 Db 661 GAAAGTATTCAGAAACAGGAAAGAGAGATGGGCTGCTTAAGGCGGCAATATATAT 720
 QY 721 CTGAGTGACACCTAAGCTTCAATGCTGAGTCTTCTCGAATGATGCGATTAACGTC 780
 Db 721 TTGAGGCGCTCATTTGACCTTAATTCACGCTGCTATTCACACGAGTGATTAACGTC 780
 QY 781 ATTGATGACATGCGACCGCATTAATCTAAGAGTAAAGCATGGAAGATTCGCGGGGCGC 840
 Db 781 ATTGATGACATTAAGCCCAATTAATTTGAAGTTAAAGCATGGAAGATTAATTCGCGGCA 840
 QY 841 CAGAAAGATTGGCAATCAATTCAGATACGATGACGATTCGCAATTAAGCGGCAATC 900

Db 841 CAAAGACTGGCAATCTAATCTAATATGAAAGCCGGTTCAATTAAGAGGAATA 900
| | | | |
Qy 901 CCAGCAATGCTGCTTGAATCTGAGGGTGCAGATTAAGAAGTTCTTAGACAA 960
| | | | |
Db 901 CCATCAATGCTGTTGTCATCCAGTGAAGGTTCCAGTTATAAGCTTCTCGACAA 960
| | | | |
Qy 961 GCAGAAATACAGGTTCTCAAGAACTGACTATCAAGATGCGATCTTCACTACCTCA 1020
| | | | |
Db 961 GAAGAAACCGAGCTTTACACAACTGACTATCATATGCGATCTTCTCGACCTCA 1020
| | | | |
Qy 1021 GCCCCCTCTATCAAGAGACACAGCGCAAGCCAGAAAGCGGCAATCAAGAGG 1077
| | | | |
Db 1021 GCCCCCTCTATCAAGACACAGAGATTGCCAAACGTAGACCAATTCGTGACG 1077
| | | | |
RESULT 9
US-09-065-999-5
; Sequence 5, Application US/09065999
; Patent No. 6118048
; GENERAL INFORMATION:
; APPLICANT: Hanson, Stephen F.
; APPLICANT: Maxwell, Douglas P.
; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: One South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/065,999
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 960296, 94754
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1651 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-065-999-5
Query Match 64.3%; Score 696.2; DB 3; Length 1651;
Best Local Similarity 77.9%; Pred. No. 1.6e-218;
Matches 839; Conservative 0; Mismatches 238; Indels 0; Gaps 0;

Qy 181 CTGTTCAGTTCGAAGTAAAGTACCAATCAGCAATTAAGATTTCTGACCTGCTCC 240
| | | | |
Db 649 CTATATCAATTCGAAGGTAAATTCCTGTCACAAATAAAGATTGTTCCACCTGGATCC 708
| | | | |
Qy 241 CCATCCCGTTCAGCAATTTCCATCCGATATTTCCAGGGAGCTTAAATCGAGCTCCGAGTC 300
| | | | |
Db 709 TCAACCGGTTCAGCACTTTTCATCCGAACTTTCAGGGAGCTTAAATCAAGTTCAAGTC 768
| | | | |
Qy 301 AAATCATATCATGACACAGACGAGATATCAATCGAATGCGGAGATTTCCAAATCGACGC 360
| | | | |
Db 769 AAGCATATCATGACACAAATGAGTCAATCGAATGAGGCAATTCAGATCGAAGCGC 828
| | | | |
Qy 361 AGATCTGCAAGAGAGGCGACAGTCTGTAATGATTAATTCATGCAAGCAATTAATGCA 420
| | | | |
Db 829 AGATCTGCAAGAGAGGTCAGAGTCTGCAACGATCTCATATGCAAGCAATTAATGCA 888
| | | | |
Qy 421 GGTTCGTTCAATCTGCTTGAAGGTTCTAAGGGAAGAACCAAGATTTGTATTA 480
| | | | |
Db 889 GATTCAATTAATCTGCTTGAACATATTAAGAAAGAACCAAGATTTGCTT 948
| | | | |
Qy 481 CAAATCATATCATGCTGCTTAACTGAAAGCAATTTGCAAGGCTCCGAACCGTGG 540
| | | | |
Db 949 CAATCATCAATCATGCTGCTTAACTGAAAGCAATTTGCAAGGCTCCGAACCGTGG 1008
| | | | |
Qy 541 GTTCTCTCAATTCAGTCTCTTCTTCACTAAGCTTCTGACGAGATGCAAGATGCGCG 600
| | | | |
Db 1009 GTTCTCTCAATTCAGTCTCTTCTTCACTAAGCTTCTGACGAGATGCAAGATGCGCG 1068
| | | | |
Qy 601 GATTAATTAATTTGGGAGCGGTTGACCGTGGCGCGGATGACCTGATGATCATGCTC 660
| | | | |
Db 1069 GAGACTAATTTGGGAGCGGTTGACCGTGGCGCGGATGACCTGATGATCATGCTC 1128
| | | | |
Qy 661 GAGGTTGATTAAGAAAGAGAGAGATGAGGCGCGGCTGCTTGAAGCCACATACTAT 720
| | | | |
Db 1129 GAAGGTGATTAAGAAAGAGAGATGAGGCGCGGCTGCTTGAAGCCACATACTAT 1188
| | | | |
Qy 721 CTGAGTGACACCTTGAATCTTAATGAGTCTTCTGAAATGATGCAATGATTAAGCTC 780
| | | | |
Db 1189 TTGAGCGGTCATTTGAGCTTAATTCACGTTCTATTCACAGCGATGGAATTCACAGCTC 1248
| | | | |
Qy 781 ATTGATGATGACGACCGGATTAATTCAGCTTAAGCACTGGAAGAAATTCGCGGGGCG 840
| | | | |
Db 1249 ATTGATGATGACGACCGGATTAATTCAGCTTAAGCACTGGAAGAAATTCGCGGGCA 1308
| | | | |
Qy 841 CAGAAAGATTGCAATCAATTTGCAAGTACGTTAGCCAGTTCAATTAAGCGGCAATC 900
| | | | |
Db 1309 CAAAGAGACTGCAATCTAATCTTAATATGAAAGCCGTTCAATTAAGAGGAATA 1368
| | | | |
Qy 901 CCAGCAATGCTGCTTGAATCTGAGGGTGCAGCTATTAAGAGTTCTTAGACAA 960
| | | | |
Db 1369 CCATCAATGCTGTTGTCATCCAGGTGAGGGTTCAGTTATAAGACTTCCCTCGACAA 1428
| | | | |
Qy 961 GCAGAAATACAGGTTCTCAAGAACTGAGTATCAAGATGCGATCTTCAACCCCTCA 1020
| | | | |
Db 1429 GAAGAAACCGAGCTTTACAACTGAGTATTAAGCAATCTTCTGTCACCTCA 1488
| | | | |
Qy 1021 GCCCCCTCTATCAAGAGACACAGCGCAAGCAAGAAAGCGGCAATCAAGAGGCG 1077
| | | | |
Db 1489 GCCCCCTCTATCAAGACACAGAGATTGCAAGCGCAATTCGTGAGAG 1545
| | | | |
RESULT 10
US-09-065-999-8
; Sequence 8, Application US/09065999
; Patent No. 6118048
; GENERAL INFORMATION:
; APPLICANT: Hanson, Stephen F.
; APPLICANT: Maxwell, Douglas P.
; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady
STREET: One South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,999
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296,94754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-065-999-8

Query Match 64.3%; Score 696.2; DB 3; Length 1894;
Best Local Similarity 77.9%; Pred. No. 1,7e-218;
Matches 833; Conservative 0; Mismatches 228; Indels 0; Gaps 0;

QY 1 ATGCCCCCAAGAAATTTAGAGTTCAAGTCAAGAACTATTCTTACTTATCCCGAG 60
DB 469 ATGCGACACCTCAAGATTAGAGTTCAAGTCAAGAACTATTCTTACTTATCCCGAG 528
QY 61 TGCCTCTATCTAAGAAAGAAAGCACTTCCCAATTACAAAACCTAATACCCCGATCAAC 120
DB 529 TGCCTCTATCTAAGAAAGAAAGCACTTCCCAATTACAAAACCTAATACCCCGATCAAC 588
QY 121 AAGAAATTCATCAAAATTTGCGAGAGCTTCATGAAATGGGGAACCTCATCTCATGTG 180
DB 589 AAAAAATTCATCAAAATTTGCGAGAGCTTCATGAAATGGGGAACCTCATCTCATGTG 648
QY 181 CTGTTCAGTTGGAAGGTAAAGTACCAATGACGAATAACAGATTCTTTCAGCTGTCTCC 240
DB 649 CTGTTCAGTTGGAAGGTAAAGTACCTGCTGCAAAATTAAGATTGTTGCACTGTATCC 708
QY 241 CCAACCGGTGACGACATTTCCATCCGAAATTTACAGGAGCTAATGAGCTCCGAGTCC 300
DB 709 TCAACGAGGTGACGACATTTCCATCCGAAATTTACAGGAGCTAATGAGCTCCGAGTCC 768
QY 301 AAATCATATATCGACAAGACGAGATATCAATCGAATGGGAGATTTCAAATCGACGCG 360
DB 769 AAGGCATATATCGACAAGATGAGTGCATCGAATGGGAGATTTCAAATCGACGCG 828
QY 361 AGATTCGCCAGAGAGGCCAGCACTGCTAATGATTCATATGCGAAAGCAATTAATGCA 420
DB 829 AGATTCGCCAGAGAGGCCAGCACTGCTAATGATTCATATGCGAAAGCAATTAATGCA 888
QY 421 GATTGCGTTCAATTTGCTTACGCGTCTTAAGGGAAGAAACCAAAAGATTTGTATTA 480
DB 889 GATTGCGTTCAATTTGCTTACGCGTCTTAAGGGAAGAAACCAAAAGATTTGTATTA 948
QY 481 CAAATCATATATCGCGCTCTAATCTGAAGCAATTTATTCGAAAGGCTCCGGAACCGTGG 540
DB 949 CAACATATATATCGCGCTCTAATCTGAAGCAATTTATTCGAAAGGCTCCGGAACCGTGG 1008
QY 541 GTTCTCTCATTTCAAGTCTCTTTCTTCACTAAGCTTCTGACGAGATGACGAATGGGCG 600

DB 1009 GTTCTCTCATTTCCGTTGTCATTCATTCATGATGTTCCGGTTGTATGCAAGATGGGT 1068
QY 601 GATATATTTTTCGGGAGCGGTGACGTCGCCGCCCGGATGACCTGAATATCATCTGC 660
DB 1069 GAGGACTATTTTCGAAAGGGGTTCGCTGCGCGCGGAAAGACCTATTAATATCATCTGC 1128
QY 661 GAGGTGATTCAGAAACAGGGAAGACGATGTGGGCGGCTGCTTAGGCCCACTAATAT 720
DB 1129 GAAGGTATTCAGAAACCGGAAGACGATGTGGGCTGCTGATTAAGACCACTAATAT 1188
QY 721 CTGAGTGACACCTAGACTTAATGCTGAGCTTTCTCGAATGATGCAATTAACGTC 780
DB 1189 TTGAGCGGTGATTTGACCTTAATTCACGCTGCTATTCACACGAGGAAATCAACGTC 1248
QY 781 ATTGATGACATTCGACCGGATTCCTAAGCTAAGACGTAAGAAATGCTGGGGGCC 840
DB 1249 ATTGATGACATTAAGCCCAATTTATTTGAATTAAGACGTAAGAAATTAATGGGCA 1308
QY 841 CAGAAAGATTGGCAATCAATTCAGTAACGTAAGCACTTCAATTAAGGCGGAATC 900
DB 1309 CAAAGGACTGGCAATCTAATCTAATATGAAAGCGGTTCAATTAAGGAGGATTA 1368
QY 901 CCAAGCAATGCTGCTTTGCAATCTGCTGAGGCTGCGACGTAATAAGATTCTTAGACAA 960
DB 1369 CCATCAATCGTGTGTGCAATCCAGGTGAGGCTTCAGTATTAAGACTTCTGACAAA 1428
QY 961 GCAGAAATACAGGTCTCAAGACGTAATGCAAGATGCAAGATGCTTATCACCTGACA 1020
DB 1429 GAAGAAACCGGACTTTACCAACTGACTTATCATATGCAATCTTGTGACCCCTACA 1488
QY 1021 GCCCCCTCTATCAAGAGACACAGGCAAGCCAGAAACGGGCAATCGAAGGCG 1077
DB 1489 GCCCCCTCTATCAAGAGACACAGGATTCGCAACGTAAGGCAATCTGTGAGCG 1545

RESULT 11
US-09-065-999-7
Sequence 7, Application US/09065999
Patent No. 6118048
GENERAL INFORMATION:
APPLICANT: Hanson, Stephen F.
TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: One South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,999
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296,94754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2072 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-065-999-7

Query Match 64.1%; Score 696.2; DB 3; Length 2072;
Best Local Similarity 77.9%; Pred. No. 1.8e-218;
Matches 839; Conservative 0; Mismatches 238; Indels 0; Gaps 0;

1 ATGCCCCCAAGAAATTTAGAGTTCAGTCAAGAACTATTCTTAATCCCAAG 60
469 ATGCGACCACTCAAGATTAGAGTTCAGTCAAGAACTATTCTTAATCCCAAG 528
61 TGTCTCTATCTTAAGAAAGACATTTCCCAATTAACAACTAAATCCCAAG 120
529 TGCCCTATACCGAAAGAAAGTTCCTTCGCACTTCAGAAAGTTCATCAGCAGCAAT 588
121 AAGAAATTCATCAAAATTTGACAGAGCTTCAGAAATTTGGGACCTCATCTCAGTG 180
589 AAAAAATTCATCAAAAGTCTGTGAGAACTCAGAAAGTGTGAGAACTCATCTTCATGCG 648
181 CTGTTCAGTTCGAAAGTAAGTACCAATGACGCAATTAACAGATTCTTCGACTGCTCC 240
649 CTATATCAATTCGAAAGTAATTCGTCTGCAAAATTAAGATTGTTGACGCTGATCC 708
241 CCAACCCGTCAGACATTTCCATCCGAATTTGAGGAGCTTAATCGAGCTCCGACGTC 300
709 TCAACCCGTCAGACATTTCCATCCGAATTTGAGGAGCTTAATCGAGCTCCGACGTC 768
301 AATATCATATGACGACGAGGACGAGATTAATGAGGAGATTTCCAAATCGACGCG 360
769 AAGCATATCATGACAAAGTAAGTACCAATGAGGAGATTTCCAAATCGACGCG 828
361 AGATCTGCAAGAGAGGAGGAGGAGTCTGTAATGATTCATATCGAAAGCATTAATGCA 420
829 AGATCTGCAAGAGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 888
421 GGTTCGTTCAATCTGCTTACGCTTCTTAAGGAAAGAAACCAAAAGTTTGTATTA 480
889 GATTCATTAATGAACTCTGACAAATTAAGAAAGAAACCAAAAGTTTGTATTA 948
481 CAAATCATATGACGACGAGGACGAGATTAATGAGGAGATTTCCAAATCGACGCG 540
949 CAAATCATATGACGACGAGGACGAGATTAATGAGGAGATTTCCAAATCGACGCG 1008
541 GTTCTCTCAATTCAGTCTCTTCTTCACTTAAGTCTTCTGACGAGATGACGAGATGCG 600
1009 GTTCTCTCAATTCAGTCTCTTCTTCACTTAAGTCTTCTGACGAGATGACGAGATGCG 1068
601 GATTAATTAATTCGAGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 660
1069 GACGACTAATTTCCGAAAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 1128
661 GAGGAGTTCAGAAAGAGGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 720
1129 GAGGAGTTCAGAAAGAGGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 1188
721 CTCAGTGCACCTTAAGTTCAGTCTTCTGATGATGATGATGATGATGATGATGATGATGAT 780
1189 TTGAGGCGGCTATTTGAGCTTATTAATCACTGATGATGATGATGATGATGATGATGATGAT 1248
781 ATTGATGACATCGCAGCGCTTAATCTTAAGGATTAAGGATTAAGGATTAAGGATTAAGGATTA 840
1249 ATTGATGACATCGCAGCGCTTAATCTTAAGGATTAAGGATTAAGGATTAAGGATTAAGGATTA 1308
841 CAGAAAGATTCAGAAAGAGGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 900
1309 CAGAAAGATTCAGAAAGAGGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 1368
901 CAGCAATCTGCTTTCAGTCTGATGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 960
1369 CAGCAATCTGCTTTCAGTCTGATGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 1428
961 GCGAAATTAAGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGT 1020

DB 1429 GAAGAAACCGAGCTTACACACTGAGTATTCATTAAGCAATCTTCGACCTCACA 1488
QY 1021 GCCCCCCCTATCAAGAGACACAGAGCAAGCAAGAAAGCGGCAATGAGAGCG 1077
DB 1489 GCCCCCCCTATCAAGAGACACAGAGTGTGCAAGCTAGAGCATTCGTGACG 1545

RESULT 12

US-08-838-151A-45
Sequence 45, Application US/08838151A
Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T
APPLICANT: Lau, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESS: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:
LENGTH: 1183 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Geminiivirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala

FEATURE:

NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-45

Query Match 64.1%; Score 694.6; DB 3; Length 1183;
Best Local Similarity 77.8%; Pred. No. 4.3e-218;
Matches 838; Conservative 0; Mismatches 239; Indels 0; Gaps 0;

1 ATGCCCCCAAGAAATTTAGAGTTCAGTCAAGAACTATTCTTAATCCCAAG 60
1 ATGCGACCACTCAAGATTAGAGTTCAGTCAAGAACTATTCTTAATCCCAAG 60
61 TGTCTCTATCTTAAGAAAGACATTTCCCAATTAACAACTAAATCCCAAG 120
1 TGCCCTATACCGAAAGAAAGTTCCTTCGCACTTCAGAAAGTTCATCAGCAGCAAT 120

QY 121 AGAATTCATCAAAATTTGACAGAGCTTCATGAAAAATGGGGAACCTCATCTCATGTG 180
DB 121 AAAAAATTCATCAAAATTTGACAGAGCTTCATGAAAAATGGGGAACCTCATCTCATGTG 180
QY 181 CTGTTCAGTTCGAAGGTAATGCAATGCAAGTAATGCAAGTTCCTGACCTGTCTCC 240
DB 181 CTGTTCAGTTCGAAGGTAATGCTGCACAAAATGTAAGATTTGCTGACCTGTCTCC 240
QY 241 CCAACCCGCTCAGACATTTTCATCCGAATTTTGAAGGAGCTAATGAGCTCCGAGCTC 300
DB 241 TCAACCAAGGTCAGACATTTTCATCCGAATTTTGAAGGAGCTAATGAGCTCCGAGCTC 300
QY 301 AAATTCATATCCGACAGACGAGATATCAATGGAATGGGAGATTTCCAAATGAGCGC 360
DB 301 AAGGATATATCCGACAGACGAGATATCAATGGAATGGGAGATTTCCAAATGAGCGC 360
QY 361 AGATCTGCAAGAGAGGCGACAGCTCTGTAATGATTCATATGCGAAGCAATTAATGCA 420
DB 361 AGATCTGCAAGAGAGGCGACAGCTCTGTAATGATTCATATGCGAAGCAATTAATGCA 420
QY 421 GGTTCGCTCAATTCGCTTACGCGTTCCTAAGGGAAGAACCAAAAGATTTGATTA 480
DB 421 GATTCAATTAATTCGCTTACGCGTTCCTAAGGGAAGAACCAAAAGATTTGATTA 480
QY 481 CAAATCATATCAATCCGCTCTAATCTGAAAGCAATTTTCGCAAGGCTCCGGAACGCTGG 540
DB 481 CAACATATCAATCCGCTCTAATCTGAAAGCAATTTTCGCAAGGCTCCGGAACGCTGG 540
QY 541 GTTCCTCAATTCGCTTACGCGTTCCTAAGGGAAGAACCAAAAGATTTGATTA 600
DB 541 GTTCCTCAATTCGCTTACGCGTTCCTAAGGGAAGAACCAAAAGATTTGATTA 600
QY 601 GATTAATTTTCGGAAGGCTGACGCTGCGCGCGGATGACCTGTAATGATCATGCTC 660
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QY 661 GAGGCTATTCAGAAAGAGGAAAGAGATGAGGCGGCTGCTGATTAAGGCTCAATATCAT 720
DB 661 GAGGCTATTCAGAAAGAGGAAAGAGATGAGGCGGCTGCTGATTAAGGCTCAATATCAT 720
QY 721 CTGAGTGAACCTGATCTCAATGCTGAGTCTTCTGAAATGATGAGTATTAACGCTC 780
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QY 781 ATTGATGACATGACCGCATTTATCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTA 840
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DB 841 CAGAAATTTGCAATCAATTTGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 900
QY 901 CCAAGCAATGCTGCTTTCGAATCTGCTGAGGCTGCAAGCTAATTAAGGCTTTAGACAA 960
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RESULT 13

US-09-065-999-6

; Sequence 6, Application US/09065999

; Patent No. 6118048

; GENERAL INFORMATION:

; APPLICANT: Hanson, Stephen F.

; APPLICANT: Maxwell, Douglas P.

;; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
;; TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESS: Charles & Brady
;; STREET: One South Pinckney Street
;; CITY: Madison
;; STATE: WI
;; COUNTRY: US
;; ZIP: 53701-2113
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/065,999
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Seay, Nicholas J.
;; REGISTRATION NUMBER: 27,386
;; REFERENCE/DOCKET NUMBER: 960296, 94754
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 608-251-5000
;; TELEFAX: 608-251-9166
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1651 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-09-065-999-6

Query Match 64.1%; Score 694.6; DB 3; Length 1651;
Best Local Similarity 77.8%; Pred. No. 5.3e-218;
Matches 838; Conservative 0; Mismatches 239; Indels 0; Gaps 0;

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DB 529 TGCCCTATACGAAAGAGAGATTTCTTCCCACTTCAAGAGATTCATACAGCAGAT 588
QY 121 AAGAAATTCATCAAAATTTGCAAGAGCTTCATGAAATGAGGAACTCATCTCATGTG 180
DB 589 AAAAAATTCATCAAAAGCTGTGAGAAAGTCACAGAGATGTAACCTCATCTTCATGCG 648
QY 181 CTGTTCAGTTCGAAGGTAATGCAATGCAAGGTAATGCAAGGTAATGCAAGGTAATGCA 240
DB 649 CTATTCATATTCGAAGGTAATGCTGTGCAAAATTAAGATTTGCAAGCTGTGATCC 708
QY 241 CCAACCCGCTCAGACATTTTCATCCGAATTTTCAAGGAGCTAATGAGCTCCGAGCTC 300
DB 709 TCAACCAAGCTCAGACATTTTCATCCGAATTTTCAAGGAGCTAATGAGCTCCGAGCTC 768
QY 301 AAATTCATATCCGACAGACGAGATATCAATGGAATGGGAGATTTCCAAATGAGCGC 360
DB 769 AAGGATATATCCGACAGACGAGATATCAATGGAATGGGAGATTTCCAAATGAGCGC 828
QY 361 AGATCTGCAAGAGAGGCGACAGCTCTGTAATGATTCATATGCGAAGCAATTAATGCA 420
DB 829 AGATCTGCAAGAGAGGCGACAGCTCTGCAAGCTCATATGCGAAGCAATTAATGCA 888
QY 421 GGTTCGCTCAATTCGCTTACGCGTTCCTAAGGGAAGAACCAAAAGATTTGATTA 480
DB 889 GATTCAATTAATTCGCTTACGCGTTCCTAAGGGAAGAACCAAAAGATTTGATTA 948
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Db 949 CAACATCACAAATCCGTTCTAATCTGAAACGATCTTCTGCAAAAGTCCGGAACATGG 1008
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 Db 1009 GTTCTTCATTTCAAGTCTCTTTCTTCACTAAGCTTCTGACGAGATGACGAATGGGCG 1068
 QY 601 GATATATTTTGGGAGGAGTGAAGCTGCGGCGCGCGGATGACCTGTAATGATATGTC 660
 Db 1069 GACGACTATTTTGGGAGGAGTGAAGCTGCGGCGCGCGGATGACCTGTAATGATATGTC 1128
 QY 661 GAGGAGTATTTCAAGAACGAGGAAGACGATGAGGCGGCGGATGACCTGTAATGATATGTC 720
 Db 1129 GAGGAGTATTTCAAGAACGAGGAAGACGATGAGGCGGCGGATGACCTGTAATGATATGTC 1188
 QY 721 CTGAGTGACACCTAGACTTCAATGCTGAGTCTTCTGATGATGTCAGATATACGTC 780
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 Db 1249 ATTGATGACATCGCACCGCATTTATCTAAGCTAAGACATGGAAGAAATGCTGGGGCC 1308
 QY 841 CAGAAAGATTTGGCAATCAAAATGCGTAAGCTGTAAGCTTCAATTAAGCGGCAATC 900
 Db 1309 CAGAAAGATTTGGCAATCAAAATGCGTAAGCTGTAAGCTTCAATTAAGCGGCAATC 1368
 QY 901 CCAAGCATCTGCTTTGCAATCTCTGATGAGGCTGCGCACTAATAAGATTTCTAGACAA 960
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 QY 961 GCAGAAATACAGCTCTCAAGAACTGCACTATCAAGAAATGCGATCTTCAATCACTTACA 1020
 Db 1429 GAAGAAATACAGCTCTCAAGAACTGCACTATCAAGAAATGCGATCTTCAATCACTTACA 1488
 QY 1021 GCCCCTCTATCAAGAGACACACAGGCAAGCCCAAGAAAGCGCAATTCAGAAAGCG 1077
 Db 1489 GCCCCTCTATCAAGAGACACACAGGCAAGCCCAAGAAAGCGCAATTCAGAAAGCG 1545

RESULT 14 US-08-838-151A-48

; Sequence 48, Application US/08838151A
 ; Patent No. 6291743

GENERAL INFORMATION:

; APPLICANT: Stout, John T
 ; APPLICANT: Luu, Hang T
 ; APPLICANT: Maxwell, Douglas
 ; APPLICANT: Ahlquist, Paul
 ; APPLICANT: Hanson, Steve
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dressler, Rockey, Milnamow & Katz
 ; STREET: Two Prudential Plaza, Suite 4700
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: U.S.A.
 ; ZIP: 60601

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/838,151A
 ; FILING DATE:

CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mueller, Lisa V
 ; REGISTRATION NUMBER: 38,978
 ; REFERENCE/DOCKET NUMBER: SVS3801P0260
 ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-616-5400
 ; TELEFAX: 312-616-5460
 ; INFORMATION FOR SEQ ID NO: 48:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1062 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: DNA (genomic)
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Bean Golden Mosaic Geminivirus
 ; STRAIN: Type II
 ; INDIVIDUAL ISOLATE: Guatemala
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..1059
 ; US-08-838-151A-48

Query Match 63.8%; Score 691.2; DB 3; Length 1062;
 Best Local Similarity 78.4%; Pred. No. 5.4e-217;
 Matches 828; Conservative 0; Mismatches 228; Indels 0; Gaps 0;

QY 1 ATGCCCCCAAGAAATTTAGAGTTCAATCAAAAGATTTCTTACTTATCCAG 60
 Db 1 ATGCCCCCAAGAAATTTAGAGTTCAATCAAAAGATTTCTTACTTATCCAGT 60
 QY 61 TGCTCTATCTAAGAGAGACATTTCCCAATTAACAAACCTAATACCCAGTCAAC 120
 Db 61 TGCTCTATCTAAGAGAGACATTTCCCAATTAACAAACCTAATACCCAGTCAAC 120
 QY 121 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAATAATGGGAGCTCATCTGATG 180
 Db 121 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAATAATGGGAGCTCATCTGATG 180
 QY 181 CTTGTTCACTTCAAGATGATCAATGACAGATTAACGATTTCTTCCAGCTGTCTCC 240
 Db 181 CTTGTTCACTTCAAGATGATCAATGACAGATTAACGATTTCTTCCAGCTGTCTCC 240
 QY 241 CCAACCCGTCACACATTTTCCATCCGAATATTCAGGAGCTTAATCGAGCTCCGAGTC 300
 Db 241 CCAACCCGTCACACATTTTCCATCCGAATATTCAGGAGCTTAATCGAGCTCCGAGTC 300
 QY 301 AAATCATPACATGACAGAGCGGAGATPACATGAAATGGGAGATTTCCAAATCGACGCG 360
 Db 301 AAATCATPACATGACAGAGCGGAGATPACATGAAATGGGAGATTTCCAAATCGACGCG 360
 QY 361 AGATCTGCCAGAGAGAGCGGAGCTGCTAATGATTCATATGCGAAAGCATTAATGCA 420
 Db 361 AGATCTGCCAGAGAGAGCGGAGCTGCTAATGATTCATATGCGAAAGCATTAATGCA 420
 QY 421 GGTTCGTTCAATCTGCTTACGCGGTTCTAAGGGAAGAACCAACCAAAAGATTTGATTA 480
 Db 421 GGTTCGTTCAATCTGCTTACGCGGTTCTAAGGGAAGAACCAACCAAAAGATTTGATTA 480
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 Db 481 CAACATCAATACATCCGCTCTTAACCTAGAACGAATATTCGCAAAAGCTCCGGAACCGTGG 540
 QY 541 GTTCTTCATTTCAAGTCTTCTTTCATCAAGTTCCTGACGAATGCGAAGTGGGCG 600
 Db 541 GTTCTTCATTTCAAGTCTTCTTTCATCAAGTTCCTGACGAATGCGAAGTGGGCG 600
 QY 601 GATATTTATTTGGGAGGAGTGAAGCTGCGCGCGCGGATGACCTTAAGTATCATCTGTC 660
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; Sequence 51: Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEtical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bean Golden Mosaic Geminiivirus
; STRAIN: Type II
; INDIVIDUAL ISOLATE: Guatemala

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1059
; US-08-838-151A-51

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Query Match 63.8%; Score 691.2; DB 3; Length 1062;
 Best Local Similarity 78.4%; Pred. No. 5,4e-217;
 Matches 828; Conservative 0; Mismatches 228; Indels 0; Gaps 0;

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Db      1 ATGCAACACCTCAAGATTTAGAGTTCAAGTCAAGAACTATTTCTTAATCTTATCCAG
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Db      301 AAGGCATATCATTCAGACAGAGATGAGTCAATCGAATGAGGAGATTTCCAAATCGACGC
Qy      361 AGATCTGCCAGAGAGAGCCAGAGTCTGTAATGATTCATTTGCGAAAGATTAATGCA
Db      361 AGATCTGCCAGAGAGAGTTCAGAGTCTGTCGCAACAGATTCATTAAGGATTAAGGCA
Qy      421 GGTTCGGTCAATCTGCTTACGCGTTCTAAGGAGAAACAAACAAAGATTTGATTA
Db      421 GATTCATTAATCTGCTTGAACATTTGAAGAGAAACAAACGAAAGTTAGTCTT
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Db      481 CAACATCAACATCCGCTCTTAATCTGAACGATCTTCGCAAAAGTCCGGAACCATGG
Qy      541 GTTCCTTCATTTCAAGTCTCTTTCACTAAGTTCCTTAAGAGATGACGAATGGCG
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Qy      601 GATTAATTTTGGAGCGGGTGAAGCTGCGCGCGGATGACCTGTAATCATCATGTC
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Qy      661 GAGGCTGATTCAGAAACAGGAAAGAGATGTGGCGCGTGCCTTAGCGCCACAATATAT
Db      661 GAAGGCTATTCAGAAACCGGACACAAATGTGGCTGTGCATTAAGAACCAATATATAT
Qy      721 CTGAGTGAACCTTAAGCTTCAATGCTGAGTCTTCTGAATGATGCGATTAAGTGC
Db      721 TTGAGCGGTGATTTGACCTTAATTCACGCTGTTATTCACCAAGGATTAACAGTGC
Qy      781 ATTGATGACATCGACCGCATTTCTAAAGCTTAAGACATGGAAGAAATGCTGGGGCC
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QY GCACAAAAATAGGCGTCCTAAAGCTGACATCTCAAGATGGATCTTCATCAGCCTACA 1020
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 Db 1021 GCGCCCTCTATCAAGAGACGACACAGCGAAGCCAA 1056

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GenCore version 5.1.6
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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	1040.8	96.1	1169	8	US-08-838-151A-17
5	1039.8	96.0	1169	8	US-08-838-151A-3
6	1033.8	95.5	1166	8	US-08-838-151A-13
7	702.2	64.8	1246	8	US-08-838-151A-15
8	696.2	64.3	1183	8	US-08-838-151A-43
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16	605.8	55.9	1056	18	US-10-633-850-63	Sequence 63, Appl
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18	605.8	55.9	1056	18	US-10-633-850-93	Sequence 93, Appl
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20	604.2	55.8	1056	18	US-10-633-850-85	Sequence 85, Appl
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37	596.2	55.1	1056	18	US-10-633-850-69	Sequence 69, Appl
38	479.4	44.3	1145	8	US-08-838-151A-19	Sequence 19, Appl
39	479.4	44.3	1145	8	US-08-838-151A-23	Sequence 23, Appl
40	479.4	44.3	1145	8	US-08-838-151A-26	Sequence 26, Appl
41	477.8	44.1	1145	8	US-08-838-151A-29	Sequence 29, Appl
42	445.6	41.1	1047	18	US-10-633-850-110	Sequence 110, App
43	444	41.0	1047	18	US-10-633-850-111	Sequence 111, App
44	418.4	38.6	2744	8	US-08-838-151A-59	Sequence 59, Appl
45	246.6	22.8	1403	8	US-08-838-151A-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-08-838-151A-1
; Sequence 1, Application US/08838151A
; Publication No. US20010011379A1
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Liu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiiviruses
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSER: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838, 151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38, 978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400

TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Gemini Virus
INDIVIDUAL ISOLATE: Florida
FEATURE:
NAME/KEY: CDS
LOCATION: 44..1127
PUBLICATION INFORMATION:
AUTHORS: Gilbertson, RL
AUTHORS: Hidayat, SH
AUTHORS: Papiomatias, EJ
AUTHORS: Rojas, MR
AUTHORS: Hou, YM
AUTHORS: Maxwell, DP
TITLE: Pseudorecombination between the infectious
TITLE: cloned DNA components of tomato mottle and bean
TITLE: dwarf mosaic geminiviruses.
JOURNAL: Jour. General Virol.
VOLUME: 74
PAGES: 23-31
DATE: 1993
US-08-838-151A-1

Query Match 96.7%; Score 1047.8; DB 8; Length 1162;
Best Local Similarity 98.0%; Pred. No. 2,4e-313;
Matches 1061; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 ATGCCCCCAAGAAATTTAGAGTTCAGTCAAGAAAGTATTTCTTAATATCCCGAG 60
DB 44 ATGCCCCCAAGAAATTTAGAGTTCAGTCAAGAAAGTATTTCTTAATATCCCGAG 103
QY 61 TGTCTCTATCTAAAGAAAGCACTTCCCAATTACAAAACCTAAATCCCGAGTCAAC 120
DB 104 TGTCTCTATCTAAAGAAAGCACTTCCCAATTACAAAACCTAAATCCCGAGTCAAT 163
QY 121 AAGAAATTCATCAAAATTTGACAGAGCTTCATCAAAATGGGAACTCTCATCTCATGTG 180
DB 164 AAGAAATTCATCAAAATTTGACAGAGCTTCATCAAAATGGGAACTCTCATCTCATGTG 223
QY 181 CTGTTCAGTTCGAAGGTAAAGTACCAATGACAGAAATAGATTCTTCAGCTGTCTCC 240
DB 224 CTGTTCAGTTCGAAGGTAAAGTACCAATGACAGAAATAGATTCTTCAGCTGTCTCC 283
QY 241 CCAACCCGGTCAAGCAATTTCCATCCGAATATTCAGGAGCTTAATGAGCTCCGAGTCC 300
DB 284 CCAACCCGGTCAAGCAATTTCCATCCGAATATTCAGGAGCTTAATGAGCTCCGAGTCC 343
QY 301 AAATTCATCAATCGAAGAGAGAGATACATCAATGGAATTTCCAAATGACAGGC 360
DB 344 AAATTCATCAATCGAAGAGAGAGATACATCAATGGAATTTCCAAATGACAGGC 403
QY 361 AGATCTGCCAGAGAGCCAGAGTCTGTAATGATTCATATGCGAAGCATTTAAATGCA 420
DB 404 AGATCTGCCAGAGAGCCAGAGTCTGTAATGATTCATATGCGAAGCATTTAAATGCA 463
QY 421 GGTTCGGTCAATCTGCTTAGCGTTCTAAAGGAGAACCAACCAAAAGATTTTGTATTA 480
DB 464 AGTTCGGTCAATCTGCTTAGCGTTCTAAAGGAGAACCAACCAAAAGATTTTGTATTA 523
QY 481 CAAATATATTAATCCGCTCTAATCTGAAGAAATATTCGCAAAAGGCTCCGGAACCGTGG 540
DB 524 CAAATATATTAATCCGCTCTAATCTGAAGAAATATTCGCAAAAGGCTCCGGAACCGTGG 583
QY 541 GTTCCTCATATTCAAGTCTCTTTCTTCACTAACGTTCTGACGAGATGACGAATGGCG 600

DB 584 GTTCCTCATATTCAAGTCTCTTTCTTACATTAAGTTCCTACAGAGATGACGAATGGCG 643
QY 601 GATTAATTTATTCGGAGCGGTGACGCTGCGCCCGCGAGATGACCTGATATCATCTGC 660
DB 644 GATTAATTTATTCGGAGCGGTGACGCTGCGCCCGAGAGACCTGATATCATCTGC 703
QY 661 GAGGTGATTCAGAAACAGGAGAGAGATGAGTGGGCGGTGCGTAAAGGCCACATTAAT 720
DB 704 GAGGTGATTCAGAAACAGGAGAGAGATGAGTGGGCGGTGCGTAAAGGCCACATTAAT 763
QY 721 CTCAGTGAACCTAGACCTTCAATGTCAGTCTTCGATGATGATGACATTAACGTC 780
DB 764 CTCAGTGAACCTAGACCTTCAATGTCAGTCTTCGATGATGATGACATTAACGTC 823
QY 781 ATTGATGACATCGCACCGCATTAATCTTAAGCTTAAGACCTGGAAGAATTCGCGGCGC 840
DB 824 ATTGATGACATCGCACCGCATTAATCTTAAGCTTAAGACCTGGAAGAATTCGCGGCGC 883
QY 841 CAGAAAGATTGGCAATCAAAATTCGCAAGTACGTAAGCCAGTCAAAATTAAGCGGAAATC 900
DB 884 CAGAAAGATTGGCAATCAAAATTCGCAAGTACGTAAGCCAGTCAAAATTAAGCGGAAATC 943
QY 901 CCAGCAATCGTGTCTTTCATCTCTGTGAGAGGTGCGAGCTATAAGAGTTCTTACAA 960
DB 944 CCAGCAATCGTGTCTTTCATCTCTGTGAGAGGTGCGAGCTATAAGAGTTCTTACAA 1003
QY 961 GCAAAATTCAGGTCTCAAAACCTGACCTATCAAGATTCGATCTTCATACCTTCACA 1020
DB 1004 GCAAAATTCAGGTCTCAAAACCTGACCTATCAAGATTCGATCTTCATACCTTCACA 1063
QY 1021 GCCCCTCTATCAAGAGACACACAGGCAAGCCAGAAACGGGCAATCGAAGGCGCAG 1080
DB 1064 GCCCCTCTATCAAGAGACACACAGGCAAGCCAGAAACGGGCAATCGAAGGCGCAG 1123
QY 1081 GGT 1083
DB 1124 GGT 1126

RESULT 2
US-08-838-151A-5
Sequence 5, Application US/08838151A
Publication No. US20010011379A1
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSER: Dresler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1169 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Gemini Virus
STRAIN: Florida
FEATURE:
NAME/KEY: CDS
LOCATION: 44..1127
US-08-838-151A-5

Query Match      96.5%; Score 1044.6; DB 8; Length 1169;
Best Local Similarity 97.8%; Pred. No. 2,4e-312;
Matches 1059; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 ATGCCCCCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTTACTTATCCAG 60
DB 44 ATGCCCCCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTTACTTATCCAG 103
QY 61 TGGCTCTATCTAAGAAAGACCTTCCCAATTACAAACCTAAATACCCAGTCAAC 120
DB 104 TGGCTCTATCTAAGAAAGACCTTCCCAATTACAAACCTAAATACCCAGTCAAC 163
QY 121 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAAATGGGGAACCTCATCTTCATGTG 180
DB 164 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAAATGGGGAACCTCATCTTCATGTG 223
QY 181 CTGTTTCAAGTTCGAAAGTAAGTACCATGCAAGAAATGAGATTTCTTGACCTGGTCTCC 240
DB 224 CTGTTTCAAGTTCGAAAGTAAGTACCATGCAAGAAATGAGATTTCTTGACCTGGTCTCC 283
QY 241 CCAACCCGTCAGACATTTCCATCCGAAATTTGAGGAGCTAAATGAGCTCCGACGTC 300
DB 284 CCAACCCGTCAGACATTTCCATCCGAAATTTGAGGAGCTAAATGAGCTCCGACGTC 343
QY 301 AAATCATATCATCGACAGAGAGAGATATCATGATGGGAGATTTCCAAATCGACGCG 360
DB 344 AAATCATATCATCGACAGAGAGAGATATCATGATGGGAGATTTCCAAATCGACGCG 403
QY 361 AGATCTGCCAGAGAGAGAGAGAGATGCTGCTAATGATTCATATGCGAAAGCATTAATGCA 420
DB 404 AGATCTGCCAGAGAGAGAGAGAGATGCTGCTAATGATTCATATGCGAAAGCATTAATGCA 463
QY 421 GGTTGGTTCAATCTGCTTAAAGGCTTCTAAGGGAAGAGACCAAGAAATTTTGTATTA 480
DB 464 GGTTGGTTCAATCTGCTTAAAGGCTTCTAAGGGAAGAGACCAAGAAATTTTGTATTA 523
QY 481 CAAATCATATCAATCCGCTCTAATCTAAGAGATATTTCCAAAGCTCCGAAACCGTGG 540
DB 524 CAAATCATATCAATCCGCTCTAATCTAAGAGATATTTCCAAAGCTCCGAAACCGTGG 583
QY 541 GTTCTCTCATATTCAGAGTCTCTTCTTCACTAAGCTTCTGACGAGATGCGAAATGGGCG 600
DB 584 GTTCTCTCATATTCAGAGTCTCTTCTTCACTAAGCTTCTGACGAGATGCGAAATGGGCG 643
QY 601 GATATATTTTGGGAGCGGAGAGCTGCGCGCGCGAGATGAGCTGTAAGTATCATGCTC 660
DB 644 GATATATTTTGGGAGCGGAGAGCTGCGCGCGCGAGATGAGCTGTAAGTATCATGCTC 703
QY 661 GAGGGTATTCAGAGAACGAGAGACGATGTGGCGGCTGTGGTGAAGCCCAATTAATAT 720
DB 704 GAGGGTATTCAGAGAACGAGAGACGATGTGGCGGCTGTGGTGAAGCCCAATTAATAT 763
QY 721 CTCAGTGAACACCTAAGCTTCAATGTGAGTCTTCTGAAATGATGTGCAATTAACGTC 780

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DB 764 CTCAGTGAACACCTAAGCTTCAATGTGAGTCTTCTGAAATGATGTGCAATTAACGTC 823
QY 781 ATTGATGACATCGACCGCATTTATCTAAGCTAAGACATGGAAGATTTGCTGGGGCC 840
DB 824 ATTGATGACATCGACCGCATTTATCTAAGCTAAGACATGGAAGATTTGCTGGGGCC 883
QY 841 CAGAAAGATTGGCAATCAAAATTTGCAAGTACGTAAGCCAGTTCAAAATTAAGCGCAATC 900
DB 884 CAGAAAGATTGGCAATCAAAATTTGCAAGTACGTAAGCCAGTTCAAAATTAAGCGCAATC 943
QY 901 CCAGCAATCGTCTTTCAGCAATCTGCTGAGGCGGCGCACTAATAAGTCTTAGACAA 960
DB 944 CCAGCAATCGTCTTTCAGCAATCTGCTGAGGCGGCGCACTAATAAGTCTTAGACAA 1003
QY 961 GCAGAAATACAGTCTCAAGAGACACAGGAGCCAGCAAGAAACGGGCAATCAGAAAGCGCAG 1020
DB 1004 GCAGAAATACAGTCTCAAGAGACACAGGAGCCAGCAAGAAACGGGCAATCAGAAAGCGCAG 1063
QY 1021 GCCCCTCTATCAAGAGACACAGGAGCCAGCAAGAAACGGGCAATCAGAAAGCGCAG 1080
DB 1064 GCCCCTCTATCAAGAGACACAGGAGCCAGCAAGAAACGGGCAATCAGAAAGCGCAG 1123
QY 1081 GGT 1083
DB 1124 GGT 1126

RESULT 3
US-08-838-151A-7
Sequence 7, Application US/08838151A
Publication No. US20010011379A1
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSER: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1169 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO

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ORIGINAL SOURCE:
 ORGANISM: Tomato Mottle Gemini Virus
 STRAIN: Florida
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 44..1127
 US-08-838-151A-7

Query Match 96.3%; Score 1043; DB 8; Length 1169;
 Best Local Similarity 97.7%; Pred. No. 7.5e-312;
 Matches 1058; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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Qy 1 ATGCCCCACCAAGAAATTTAGAGTCAAGTCAAGAAAGTATTTCTTAATATATCCAG 60
Db 44 ATGCCCCACCAAGAAATTTAGAGTCAAGTCAAGAAAGTATTTCTTAATATATCCAG 103
Qy 104 TGGCTTTGTCTAAAGAAAGCACTTTCCCAATTAACAAAACCTAAATATCCAGTCAAT 163
Db 121 AAGAAATTCCTCAAAATTTGAGAGAGCTTCATGAAATGAGGAACTCTCATCTCCATGTG 180
Qy 164 AAGAAATTCCTCAAAATTTGAGAGAGCTTCATGAAATGAGGAACTCTCATCTCCATGTG 223
Db 181 CTGTTCAAGTTCGAAGGTAAGTCAATGCAAGTAAAGATTTCTTCAAGTCTGCTCC 240
Qy 224 CTGTTCAAGTTCGAAGGTAAGTCAATGCAAGTAAAGATTTCTTCAAGTCTGCTCC 283
Db 241 CCAACCCGTCAGACATTTTCATCCGAATATTCAGGAGCTAAATGAGCTCCGACGTC 300
Qy 284 CCAACCCGTCAGACATTTTCATCCGAATATTCAGGAGCTAAATGAGCTCCGACGTC 343
Db 301 AAATCATACATCCGACAGGAGAGATACATGCAATGAGGAGATTTCCAATGAGAGG 360
Qy 344 AAATCATACATCCGACAGGAGAGATACATGCAATGAGGAGATTTCCAATGAGAGG 403
Db 361 AGATCTGCGCAGAGAGGCGCAGAGTCTGTAATGATTCATATGCGAAGATTAATGCA 420
Qy 404 AGATCTGCGCAGAGAGGCGCAGAGTCTGTAATGATTCATATGCGAAGATTAATGCA 463
Db 421 GGTTCGGTTCATTTGCTTAAAGCGGTTCTTAAAGGAAACCAAAAGATTTGTAATTA 480
Qy 464 AGTTCGGTTCATTTGCTTAAAGCGGTTCTTAAAGGAAACCAAAAGATTTGTAATTA 523
Db 481 CAAATCATACATCCGCTCAACCTAAGAAAGATTTTCGAAAGGCTCCGGAACCGTGG 540
Qy 524 CAAATCATACATCCGCTCAACCTAAGAAAGATTTTCGAAAGGCTCCGGAACCGTGG 583
Db 541 GTTCCTTCATTTCAAGTCTCTTTCTTCACTAAACGTTCTGCGAATGAGAAATGGGCG 600
Qy 584 GTTCCTTCATTTCAAGTCTCTTTCTTCACTAAACGTTCTGCGAATGAGAAATGGGCG 643
Db 601 GATTAATTTTTCGGGAGCGGTCGAGCTGCGCGCGCGGATGACCTGTAAGTATCATGTC 660
Qy 644 GATTAATTTTTCGGGAGCGGTCGAGCTGCGCGCGCGGATGACCTGTAAGTATCATGTC 703
Db 661 GAGGGTATTCAGAAACAGGGAAGAGATGAGGCGGCTGTTAGGCGCAACATAATAT 720
Qy 704 GAGGGTATTCAGAAACAGGGAAGAGATGAGGCGGCTGTTAGGCGCAACATAATAT 763
Db 721 CTCAGTGAACCTAGACCTTCAATGTCGAGTCTTCTCGATGATGTCAGTATTAACGTC 780
Qy 764 CTCAGTGAACCTAGACCTTCAATGTCGAGTCTTCTCGATGATGTCAGTATTAACGTC 823
Db 781 ATTGATGACATCCGACCGCATTTCTTAAAGTAAAGCACTGGAAGAAATGCTGGGGCC 840
Qy 824 ATTAAATACATCGACCGCATTTCTTAAAGTAAAGCACTGGAAGAAATGCTGGGGCC 883
Db 841 CAGAAAGATTCGAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 900
Qy 884 CAGAAAGATTCGAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 943
Db 901 CAGCAATCGTGTTCGAAATCTGTGTGAGGGTGCAGCTAATAAGATTTCTTAGACAAA 960
  
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Db 944 CAGCAATCGTGTTCGAAATCTGTGTGAGGGTGCAGCTAATAAGATTTCTTAGACAAA 1003
Qy 961 GCAGAAATACAGGTCCTCAAGAACTGACATATCAAGATGCAATCTTCAATCACTCCACA 1020
Db 1004 GCAGAAATACAGGTCCTCAAGAACTGACATATCAAGATGCAATCTTCAATCACTCCACA 1063
Qy 1021 GCCCCCCCTTATCAAGAGACACACAGGCAAGCCAAAGAAACGGGCAATCAGAAAGCGCAG 1080
Db 1064 GCCCCCCCTTATCAAGAGACACACAGGCAAGCCAAAGAAACGGGCAATCAGAAAGCGCAG 1123
Qy 1081 GGT 1083
Db 1124 GGT 1126
  
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```

RESULT 4
US-08-838-151A-17/c
Sequence 17, Application US/08838151A
Publication No. US20010011379A1
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESS: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2602 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle GeminiVirus
STRAIN: Florida
US-08-838-151A-17
  
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Query Match 96.1%; Score 1040.8; DB 8; Length 2602;
 Best Local Similarity 98.0%; Pred. No. 5.5e-311;
 Matches 1054; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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Qy 8 CACCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTTAATATATCCAGTCTCTC 67
Db 2602 CACCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTTAATATATCCAGTCTCTC 2543
  
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QY 68 TATCTAAGAGAGACGCTTCCCAATTACAAAACCTAAATACCCTGTCACAGAAAT 127
DB 2542 TGCTAAGAGAGAGACGCTTCCCAATTACAAAACCTAAATACCCTGTCACAGAAAT 2483
QY 128 TCATCAAAATTTGAGAGAGCTTATGAAATGGGGAACCTCATCTCCATGCTGTTTC 187
DB 2482 TCATCAAAATTTGAGAGAGCTTATGAAATGGGGAACCTCATCTCCATGCTGTTTC 2423
QY 188 AGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 247
DB 2422 AGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2263
QY 248 GGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 307
DB 2362 GGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2303
QY 308 ACATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 367
DB 2302 ACATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2243
QY 368 CCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 427
DB 2242 CCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2183
QY 428 TTCAATCTGCTTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 487
DB 2182 TTCAATCTGCTTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2123
QY 488 ATAAACATCGCTCTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 547
DB 2122 ATAAACATCGCTCTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2063
QY 548 CATTTCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 607
DB 2062 CATTTCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2003
QY 608 ATTTTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 667
DB 2002 ATTTTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1943
QY 668 ATTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 727
DB 1942 ATTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1883
QY 728 GACACCTAGACTTCAATGAGTGAAGTCTTCAATGAGTGAAGTGAAGTGAAGTGAAG 787
DB 1882 GACACCTAGACTTCAATGAGTGAAGTCTTCAATGAGTGAAGTGAAGTGAAGTGAAG 1823
QY 788 ACATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 847
DB 1822 ACATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1763
QY 848 ATTGGCAATCAAAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 907
DB 1762 ATTGGCAATCAAAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1703
QY 908 TCGTGTCTTTCGAAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 967
DB 1702 TCGTGTCTTTCGAAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1643
QY 968 ATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1027
DB 1642 ATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1583
QY 1028 TCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1083
DB 1582 TCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1527

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RESULT 5
 US-08-838-151A-3
 ; Sequence 3, Application US/08838151A
 ; Publication No. US20010011379A1

```

? GENERAL INFORMATION:
? APPLICANT: Stout, John T
? APPLICANT: Lau, Hang T
? APPLICANT: Maxwell, Douglas
? APPLICANT: Ahlquist, Paul
? APPLICANT: Hanson, Steve
? TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
? TITLE OF INVENTION: Genes
? NUMBER OF SEQUENCES: 63
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Dresler, Rocky, Milnamow & Katz
? STREET: Two Prudential Plaza, Suite 4700
? CITY: Chicago
? STATE: Illinois
? COUNTRY: U.S.A.
? ZIP: 60601
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/838,151A
? FILING DATE:
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? NAME: Mueller, Lisa V
? REGISTRATION NUMBER: 38,978
? REFERENCE/DOCKET NUMBER: SVS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5400
? TELEFAX: 312-616-5460
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1169 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Tomato Mottle Gemini Virus
? STRAIN: Florida
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 44..1127
? PUBLICATION INFORMATION:
? AUTHORS: Gilbertson, RL et al.
? TITLE: Pseudorecombination between the infectious
? TITLE: cloned DNA components of tomato mottle and bean
? TITLE: dwarf mosaic geminivirus.
? JOURNAL: Journal of General Virology
? VOLUME: 74
? PAGES: 23-31
? DATE: 1993
?
? US-08-838-151A-3
?
? Query Match 96.0%; Score 1039.8; DB 8; Length 1169;
? Best Local Similarity 97.5%; Pred. No. 7.3e-111;
? Matches 1056; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

```

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QY 1 ATGCCCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
DB 44 ATGCCCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 103
QY 61 TGCTCTCTATCTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 104 TGCTCTCTCTATCTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 163
QY 121 AAGAAATTCATCAAAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 164 AAGAAATTCATCAAAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 223

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QY 181 CTTGTCAGTTCGAGGTAAGTACCAATGACGAATAACAGATTCTTCCAGCTGCTCC 240
Db 224 CTTGTCAGTTCGAGGTAAGTACCAATGACGAATAACAGATTCTTCCAGCTGCTCC 283
QY 241 CCAACCCGGTCAGACATTTTCATCCGAATATTCAGGAGCTTAATGAGCTCCGAGTC 300
Db 284 CCAACCCGGTCAGACATTTTCATCCGAATATTCAGGAGCTTAATGAGCTCCGAGTC 343
QY 301 AAATCATATCCGACAGACGAGATCAATCGAATGGGAGATTTTCAATGACGCGC 360
Db 344 AAATCGTACATCGACAGACGAGATCAATCGAATGGGAGATTTTCAATGACGCGC 403
QY 361 AGATCTGCGAGAGGCGACGAGCTGCTAATGATTCATATGCGAAGCATTTAAATGCA 420
Db 404 AGATCTGCGAGAGGCGACGAGCTGCTAATGATTCATATGCGAAGCATTTAAATGCA 463
QY 421 GATTGCTCAATCTGCTTACGCGTTCTAAGGGAAGAACCAACCAAGATTTGTATTA 480
Db 464 AGTTGCTCAATCTGCTTACGCGTTCTAAGGGAAGAACCAACCAAGATTTGTATTA 523
QY 481 CAAATATATATCCGCTCTAATCTTGAACGAATATTCGAAAGCTCCGGAACCGTGG 540
Db 524 CAAATATATATCCGCTCTAATCTTGAACGAATATTCGAAAGCTCCGGAACCGTGG 583
QY 541 GTTCCTCATTTCAAGTCTCTTTCACTAAGCTTCTGAGAGATGACGAATGGGCG 600
Db 584 GTTCCTCATTTCAAGTCTCTTTCACTAAGCTTCTGAGAGATGACGAATGGGCG 643
QY 601 GATATATATTTTGGGAGCGGTGACGCTGCGCGCGGATGACCTGTATGATCATGTC 660
Db 644 GATATATATTTTGGGAGCGGTGACGCTGCGCGCGGATGACCTGTATGATCATGTC 703
QY 661 GAGGCTATTTCAAGAGAGGAGACGATGGGCGGCTGTTAAGCCCAATATAT 720
Db 704 GAGGCTATTTCAAGAGAGGAGACGATGGGCGGCTGTTAAGCCCAATATAT 763
QY 721 CTCAGTGAACCTAGACTTCAATGTCAGAGTCTTCTGAAATGATGACGATATACGTC 780
Db 764 CTCAGTGAACCTAGACTTCAATGTCAGAGTCTTCTGAAATGATGACGATATACGTC 823
QY 781 ATTGATGACATCGACCGCATTTCTAAGCTAAGCACTGGAAGAAATGCTGGGGCC 840
Db 824 ATTGATGACATCGACCGCATTTCTAAGCTAAGCACTGGAAGAAATGCTGGGGCC 883
QY 841 CAGAAATATGCGAATTAATGCAATGCGTAAGCACTGTAATTAATTAAGGCGAATC 900
Db 884 CAGAAATATGCGAATTAATGCAATGCGTAAGCACTGTAATTAATTAAGGCGAATC 943
QY 901 CCAAGCATCGTCTTTGCAATCTGTCAGGAGTCCAGCTATTAAGATTCTTGAACAA 960
Db 944 CCAAGCATCGTCTTTGCAATCTGTCAGGAGTCCAGCTATTAAGATTCTTGAACAA 1003
QY 961 GCAAGAAATATCAGGTCTCAAGAACTGATCTATCAAGATGCGATCTTCACTCA 1020
Db 1004 GCAAGAAATATCAGGTCTTAAAGAACTGATCTATCAAGATGCGATCTTCACTCA 1063
QY 1021 GCCCCCCCTATCAAGAGAGACACAGCAAGCCCAAGACCGGCAATCGAAGCGCAG 1080
Db 1064 GCCCCCCCTATCAAGAGAGACACAGCAAGCCCAAGACCGGCAATCGAAGCGCAG 1123
QY 1081 GGT 1083
Db 1124 GGT 1126

RESULT 6

US-08-838-151A-13
; Sequence 13, Application US/08838151A

; Publication No. US2001011379A1

; GENERAL INFORMATION:

; APPLICANT: Stout, John T

; APPLICANT: Luu, Hang T

APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSER: Dresler, Rocky, Milamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1166 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle GeminiVirus
INDIVIDUAL ISOLATE: Florida
FEATURE:
NAME/KEY: CDS
LOCATION: 44..436
US-08-838-151A-13
Query Match 95.5%; Score 1033.8; DB 8; Length 1166;
Best Local Similarity 97.6%; Pred. No. 5.3e-309;
Matches 1061; Conservative 0; Mismatches 22; Indels 4; Gaps 1;
QY 1 ATGCCCCCAGCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTTATCCCTTCCAG 60
Db 44 ATGCCCCCAGCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTTATCCCTTCCAG 103
QY 61 TGTCTCTATCTAAGAGAGACATTTCCCAATTACAAAACCTTAATACCCAGTCAAC 120
Db 104 TGTCTCTTGTCTAAGAGAGACATTTCCCAATTACAAAACCTTAATACCCAGTCAAT 163
QY 121 AAGAAATTCATCAAAATTTTCAGAGAGCTTCAAGAAATGGGGAACCTCATCTCCAGTG 180
Db 164 AAGAAATTCATCAAAATTTTCAGAGAGCTTCAAGAAATGGGGAACCTCATCTCCAGTG 223
QY 181 CTTGTCAGTTCGAGGTAAGTACCAATGACGAATAACAGATTCTTCCAGCTGCTCC 240
Db 224 CTTGTCAGTTCGAGGTAAGTACCAATGACGAATAACAGATTCTTCCAGCTGCTCC 283
QY 241 CCAACCCGGTCAGACATTTTCATCCGAATATTCAGGAGCTTAATGAGCTCCGAGTC 300
Db 284 CCAACCCGGTCAGACATTTTCATCCGAATATTCAGGAGCTTAATGAGCTCCGAGTC 343
QY 301 AAATCATATCCGACAGACGAGATCAATCGAATGGGAGATTTTCAATGACGCGC 360
Db 344 AAATCGTACATCGACAGACGAGATCAATCGAATGGGAGATTTTCAATGACGCGC 403

QY 361 A----GATCTGCCAGAGGAGGCGCAGCAGTCTGCTAATGATTCATATGCGAAGCATTAA 416
DB 404 AGATCATCTGCCAGAGGAGGCGCAGCAGTCTGCTAATGATTCATATGCGAAGCATTAA 463
QY 417 TCGAGTTCGCTTCATCTGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTAC 476
DB 464 TCGAGTTCGCTTCATCTGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTAC 523
QY 477 ATTACAAAATCATACATCCGCTCTAAGCTTAAAGCAAGATATGCGAAGGCTCCGGAACC 536
DB 524 ATTACAAAATCATACATCCGCTCTAAGCTTAAAGCAAGATATGCGAAGGCTCCGGAACC 583
QY 537 GTGGGTTCTCTCATCTTCAAGTCTCTTCTTCACTAACGTTCTCGACGAGATGCAAGATG 596
DB 584 GTGGGTTCTCTCATCTTCAAGTCTCTTCTTCACTAACGTTCTCGACGAGATGCAAGATG 643
QY 597 GGGGGAATTAATTTTGGGGAAGGCTGACGCTGCGCGCGCGGATGAGCTTGAATGATCAT 656
DB 644 GGGGGAATTAATTTTGGGGAAGGCTGACGCTGCGCGCGCGGATGAGCTTGAATGATCAT 703
QY 657 CGTCGAGGCTGATTCAGAAACAGGGAAGAGATGTGGGCGCTGAGCTTAAAGCCACATAA 716
DB 704 CGTCGAGGCTGATTCAGAAACAGGGAAGAGATGTGGGCGCTGAGCTTAAAGCCACATAA 763
QY 717 CTATCTCAGTGAACACCTAGACTTCAATGCTGCAATGCTTCTCGAATGATGCAATATA 776
DB 764 CTATCTCAGTGAACACCTAGACTTCAATGCTGCAATGCTTCTCGAATGATGCAATATA 823
QY 777 CGTCATGATGATGACGACCGCATTAATCTAAAGCTTAAAGCAAGATATGCGAAGGCT 836
DB 824 CGTCATGATGATGACGACCGCATTAATCTAAAGCTTAAAGCAAGATATGCGAAGGCT 883
QY 837 GGGCCGAAAGATTTGGCAATCAATTGCAAGTACGATGCGTAAAGCCAGTTCAATTAAGCGG 896
DB 884 GGGCCGAAAGATTTGGCAATCAATTGCAAGTACGATGCGTAAAGCCAGTTCAATTAAGCGG 943
QY 897 AATCCAGCAATCGTGTCTTTCATCTCTGCTGAGGCTGCGAAGCTTAAAGATTTCTTGA 956
DB 944 AATCCAGCAATCGTGTCTTTCATCTCTGCTGAGGCTGCGAAGCTTAAAGATTTCTTGA 1003
QY 957 CAAGAGCAAAATACAGTCTTCAAGAACTGCAATTAAGAAATGCGATCTTCAACCCCT 1016
DB 1004 CAAGAGCAAAATACAGTCTTCAAGAACTGCAATTAAGAAATGCGATCTTCAACCCCT 1063
QY 1017 CACAGCCCCCTCTATCAAGAGACACACAGCAAGCCCAAGAAACGGGCAATCAGAAAGC 1076
DB 1064 CACAGCCCCCTCTATCAAGAGACACACAGCAAGCCCAAGAAACGGGCAATCAGAAAGC 1123
QY 1077 GCAGGGT 1083
DB 1124 GCAGGGT 1130

RESULT 7
US-08-838-151A-15
Sequence 15, Application US/08838151A
Publication No. US20010011379A1
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.

ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1246 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Geminiivirus
STRAIN: Florida
PUBLICATION INFORMATION:
AUTHORS: Gilbertson, RL
AUTHORS: Hidayat, SH
AUTHORS: Papadimitriou, EJ
AUTHORS: Rojas, MR
AUTHORS: Hou, YM
AUTHORS: Maxwell, DP
TITLE: Pseudorecombination between the infectious
TITLE: Cloned DNA components of tomato mottle and bean
TITLE: dwarf mosaic Geminiiviruses.
JOURNAL: Journal of General Virology
VOLUME: 74
PAGES: 23-31
DATE: 1993
US-08-838-151A-15

Query Match 64.8%; Score 702.2; DB 8; Length 1246;
Best Local Similarity 98.2%; Pred. No. 2,8e-206;
Matches 710; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 361 AGATCTGCCAGAGGAGGCGCAGCAGTCTGCTAATGATTCATATGCGAAGCATTAAATGCA 420
DB 1 AGATCTGCCAGAGGAGGCGCAGCAGTCTGCTAATGATTCATATGCGAAGCATTAAATGCA 60
QY 421 GGTTCGCTCAATCTGCTTAAAGGCTTAAAGGCAAGCAACCAAAAGTTTGTATT 480
DB 61 AGTTGCTCAATCTGCTTAAAGGCTTAAAGGCAAGCAACCAAAAGTTTGTATT 120
QY 481 CAAATCATACATCCGCTCTAAGCTTAAAGCAAGATATGCGAAGGCTCCGGAACGCTG 540
DB 121 CAAATCATACATCCGCTCTAAGCTTAAAGCAAGATATGCGAAGGCTCCGGAACGCTG 180
QY 541 GTTCTCTCAATCAAGTCTTCTTCACTAACGTTCTCGACGAGATGCAAGATGCGG 600
DB 181 GTTCTCTCAATCAAGTCTTCTTCACTAACGTTCTCGACGAGATGCAAGATGCGG 240
QY 601 GATTAATTTTGGGGAAGGCTGACGCTGCGCGCGGATGAGACCTGTAAGTATCATGCTG 660
DB 241 GATTAATTTTGGGGAAGGCTGACGCTGCGCGCGGATGAGACCTGTAAGTATCATGCTG 300
QY 661 GAGGCTGATTCAGAAACAGGGAAGAGATGTGGGCGCTGAGCTTAAAGCCACATACTAT 720
DB 301 GAGGCTGATTCAGAAACAGGGAAGAGATGTGGGCGCTGAGCTTAAAGCCACATACTAT 360

QY 721 CTCAGTGAACACCTAGCTTCAATGATGAGTCTTCTGAAATGATGACAGTATTAACGTC 780
DB 361 CTCAGTGAACACCTAGCTTCAATGATGAGTCTTCTGAAATGATGACAGTATTAACGTC 420
QY 781 ATTGATGACATCGACCGCATTTATCTAAAGCTAAAGCATGGAAGAAATGCTGGGGCC 840
DB 421 ATTGATGACATCGACCGCATTTATCTAAAGCTAAAGCATGGAAGAAATGCTGGGGCC 480
QY 841 CAGAAATGTCGCAATGAAATGGAATGCAAGTAAAGCAGTCAATTAAGGGGAAATC 900
DB 481 CAGAAATGTCGCAATGAAATGGAATGCAAGTAAAGCAGTCAATTAAGGGGAAATC 540
QY 901 CAGCAATCGTCTTTCATTCCTGATGAGGTCCTGATTAAGAGTTCTTGAACAAA 960
DB 541 CAGCAATCGTCTTTCATTCCTGATGAGGTCCTGATTAAGAGTTCTTGAACAAA 600
QY 961 GCAGAAATACAGGTCCTCAAGACCTGATCTAAAGAAATGCAATCTTCAATCAGCCCTACA 1020
DB 601 GCAGAAATACAGGTCCTCAAGACCTGATCTAAAGAAATGCAATCTTCAATCAGCCCTACA 660
QY 1021 GCGCCCTCTATCAAGAGACACAGCAAGCCAAAGGCGCATCAAGAGCGCAG 1080
DB 661 GCGCCCTCTATCAAGAGACACAGCAAGCCAAAGGCGCATCAAGAGCGCAG 720
QY 1081 GGT 1083
DB 721 GGT 723

RESULT 8

US-08-838-151A-43

Sequence 43, Application US/08838151A

Publication No. US20010011379A1

GENERAL INFORMATION:

APPLICANT: Stout, John T

APPLICANT: Luu, Hang T

APPLICANT: Maxwell, Douglas

APPLICANT: Ahlquist, Paul

APPLICANT: Hanson, Steve

TITLE OF INVENTION: Transgenic Plants Expressing Geminitivirus

TITLE OF INVENTION: Genes

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Rocky, Milnamow & Katz

STREET: Two Prudential Plaza, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838, 151A

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Mueller, Lisa V

REGISTRATION NUMBER: 38,978

REFERENCE/DOCKET NUMBER: SVS3801P0260

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400

TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 1183 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Geminitivirus
STRAIN: Type II Isolates
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
PUBLICATION INFORMATION:
AUTHORS: Faria, JC
AUTHORS: Gilbertson, RL
AUTHORS: Hanson, SF
AUTHORS: Morales, FJ
AUTHORS: Ahlquist, P
AUTHORS: Loniello, AO
AUTHORS: Maxwell, D
TITLE: Bean Golden Mosaic Geminitivirus Type II
TITLE: Isolates from the Dominican Republic and
TITLE: Guatemala: Nucleotide Sequences, Infectious
TITLE: Pseudorecombinants, and Phylogenetic Relationships
JOURNAL: Phycopathology
VOLUME: 84
ISSUE: 3
PAGES: 321-329
DATE: 1994
US-08-838-151A-43

Query Match 64.3%; Score 696.2; DB 8; Length 1183;

Best Local Similarity 77.9%; Pred. No. 2e-204;

Matches 839; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

QY 1 ATGCCCCCAACCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCCTACTTATCCCGAG 60
DB 1 ATGCCCCCAACCTCAAGATTTAGAGTTCAGTCAAGAACTATTTCCTACTTATCCCGAG 60
QY 61 TGCCTCTATCTAAAGAGAGCACTTCCCAATTACAAAACCTTAATACCCAGTCAAC 120
DB 61 TGCCTCTATCTAAAGAGAGCACTTCCCGAATTACAAAACCTTAATACCCAGTCAAC 120
QY 121 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAAATGAGGAACCTCATTCCTCAATG 180
DB 121 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAAATGAGGAACCTCATTCCTCAATG 180
QY 181 CTGCTCAGTTCGAAAGTAAAGTACCAATGACAGCAATACAGATTCCTCGACCTGCTCC 240
DB 181 CTGCTCAGTTCGAAAGTAAAGTACCAATGACAGCAATACAGATTCCTCGACCTGCTCC 240
QY 241 CAAACCCGTCAGACATTTCCATCCGAATATTCAGGAGCTTAATGAGCTCCGACGTC 300
DB 241 CAAACCCGTCAGACATTTCCATCCGAATATTCAGGAGCTTAATGAGCTCCGACGTC 300
QY 301 AATCATATCATCGACAGAGAGAGATGCAATGCAATGAGGAGATTTCCAAATCGAGCGC 360
DB 301 AATCATATCATCGACAGAGAGAGATGCAATGCAATGAGGAGATTTCCAAATCGAGCGC 360
QY 361 AAGGCAATACATCAAGAAAGATGATGATGCAATGCAATGCAATGCAATGCAATGCAATG 420
DB 361 AAGGCAATACATCAAGAAAGATGATGATGCAATGCAATGCAATGCAATGCAATGCAATG 420
QY 421 GATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 421 GATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 481 CAAAT 540
DB 481 CAAAT 540
QY 541 GTTCCTCATATTAAGTCTCTTCTTCACTAAGTTCCTGACAGAGATGAGAGATGAGAGG 600
DB 541 GTTCCTCATATTAAGTCTCTTCTTCACTAAGTTCCTGACAGAGATGAGAGATGAGAGG 600
QY 601 GATTAATTAATTTGGGAGCGGAGTGAAGTGCAGCGCGCGGATGAGACTGTAATATATATGTC 660
DB 601 GATTAATTAATTTGGGAGCGGAGTGAAGTGCAGCGCGCGGATGAGACTGTAATATATATGTC 660


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Db      601 GACGACTATTGCGAAGGGGTTCCGCTGCCGCCGGAAGACCTATTAGTATCATCTC 660
Qy      661 GAGGATGATTCAGAAACAGGAGACGATGTGGCGCGTCGTTAGGCCACATTAATAT 720
        |||
Db      661 GAAGGATTCAGAAACCGAAGACAAATGTGGCTGTGTCATTAGACACATTAATAT 720
Qy      721 CTGAGTGACACTAGACTTCAATTCGTGAGTCTTTCGAATGTGCAATTAACGTC 780
        |||
Db      721 TTGAGCGGTCATTTGGACTTTAATTCACGTGTCTATTCACAGAGTGGAATCAACGTC 780
Qy      781 ATTGATGACATGCGACCGCATTAATCTTAAGCTAAGACGGAAGAAATGTGGGGGCC 840
        |||
Db      781 ATTGATGACATTAAGCCCAATTAATTTGAATTAAGACATGGAAGAACTAATTTGGGCA 840
Qy      841 CAGAAAGATTGGCAATCAATTCAGTAAGCTAAGCAAGTTCATTAATTAAGGCGGATC 900
        |||
Db      841 CAAAGAGCTGGCAATCTAATCTGAATTAATGAAGCGGTTCAATTAAGAGGAAATA 900
Qy      901 CCGCAATCTGCTTTGCAATCTCTGAGAGGTGCCAGCTATAAGAGTTCTTAGACAA 960
        |||
Db      901 CCGTCAATCTGTGTGGCAATCCAGGTGAGGGTTCAGTTATAAGACTTCTCGACAA 960
Qy      961 GCAGAAATACAGGTCTCAAGAACTGACTATCAAGAAATGCAATCTTCACTCCGAC 1020
        |||
Db      961 GAAGAAACCGAGCTTACCACTGACATTAATCATATGCAATCTTCTGACCTTCACA 1020
Qy      1021 GCCCCTCTATCAAGAGACACACAGGCAAGCCAGCAATCGGCAATCGAAGGCG 1077
        |||
Db      1021 GCCCCTCTATCAAGAGACACACAGGATTTGCCAAACGTAAAGCCATTGTGTGAG 1077

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RESULT 9

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US-08-838-151A-45
; Sequence 45, Application US/08838151A
; Publication No. US20010011379A1
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1183 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular

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; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bean Golden Mosaic Geminivirus
; STRAIN: Type II
; INDIVIDUAL ISOLATE: Guatemala
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1059
; US-08-838-151A-45

Query Match      64.1%; Score 694.6; DB 8; Length 1183;
Best Local Similarity 77.8%; Pred. No. 6,2e-204;
Matches 838; Conservative 0; Mismatches 239; Indels 0; Gaps 0;

Qy      1 ATGCCCCCAACAAAGAAATTTAGATGTTCAAGTCAAAAGACTAATTTCTTAATTCACAG 60
        |||
Db      1 ATGCAACACCTCAAAAGATTTAGAGTTCAAGTCAAAAGACTAATTTCTTAATTCACAG 60
Qy      61 TGCTCTATCTTAAGAAAGACACTTTCCTCAATTAACAAACCTTAATACCCAGTCAC 120
        |||
Db      61 TGCCCTATACCGAAGAAAGAGTTCTTGGCAACTTCAAGAAATTCATACAGCAGAAAT 120
Qy      121 AAGAAATTCACAAATTTGCAAGAGCTTCATGAAGAAATGGGAACTCATCTCCATGTG 180
        |||
Db      121 AAAAAATTCATCAAGTCTGTGAGAAAGTCACAGAAATGTGAACCTCATCTTCATGCG 180
Qy      181 CTGTTCAGTGGAAAGTAAGTACCAATGACAGAAATTAAGATTTCTTCGACCTGTCTCC 240
        |||
Db      181 CTATTCAATTCAGAGTAATTTGTTCTGCAAAATTAAGATTTGTTCACTGGTATCC 240
Qy      241 CCAACCCGTCAGACATTTCCATCCGAATTTCAAGGAGCTTAATCGAGCTCCAGTC 300
        |||
Db      241 TCAACGAGTCAGACACTTTCATCCGAACTTCAAGGAGCTTAATCGAGCTCCAGTC 300
Qy      301 AATCATCATCGACAAAGAGCGAATACATGAATGGGAGATTTCCAAATCGACGCG 360
        |||
Db      301 AAGCAATACATCGACAAAGAGTGAATGACATGAATGGGAGCAATTCGAAGTCGACGCG 360
Qy      361 AGATTCGCCAGAGAGAGGCGCAGCTGCTGAATGATTCATATGCGAAGCATTAATGCA 420
        |||
Db      361 AGATTCGCAAGAGAGAGTGAAGCTGCGCAAGACTCATATGCAAGGCAATTAACGCA 420
Qy      421 GGTTCGATTCATCTGCTTGAAGCGTCTTAAGGAAACCAACAAAGATTTGTATTA 480
        |||
Db      421 GATTCAATGAATCTGCTTGAATGAATGAAGAAACCAACGAAGTTAGTGTCTT 480
Qy      481 CAAATCATTAATCTGCTTGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 540
        |||
Db      481 CAACATCACAAATCTGCTTGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 540
Qy      541 GTTCTCAATTTCAAGTCTCTTTCATCACTAAGTCTCTGACGAGATGACGAATGGGCG 600
        |||
Db      541 GTTCTCAATTTCTGTTGATCATATTCGCAATGTTCCGTTTATGCAAGATGGGTT 600
Qy      601 GATTAATTAATTTGGGAGCGGTGAAGCTGCGCGCGCGAGTAAGCTTAATGATCATGTC 660
        |||
Db      601 GACGACTAATTTGGAGAGGGGTTCCGCTGCGCGCGCGGAAAGACTTAATGATCATGTC 660
Qy      661 GAGGATGATTCAGAAACAGGAGACGATGTGGCGCGTCGTTAGGCCACATTAATAT 720
        |||
Db      661 GAAGGATTCAGAAACCGAAGACAAATGTGGCTGTGTCATTAGACACATTAATAT 720
Qy      721 CTGAGTGACACTAGACTTCAATTCGTGAGTCTTTCGAATGTGCAATTAACGTC 780
        |||
Db      721 TTGAGCGGTCATTTGGACTTTAATTCACGTGTCTATTCACAGAGTGGAATCAACGTC 780
Qy      781 ATTGATGACATGCGACCGCATTAATCTTAAGCTAAGACGGAAGAAATGTGGGGGCC 840
        |||
Db      781 ATTGATGACATTAAGCCCAATTAATTTGAATTAAGACATGGAAGAACTAATTTGGGCA 840
Qy      841 CAGAAAGATTGGCAATCAATTCAGTAAGCTAAGCAAGTTCATTAATTAAGGCGGATC 900

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Db 841 CAAAGAGCTGGCATCTAATCTAATATGAGAAAGCCGGTTCAAATTAAGAGGAATA 900
Qy 901 CCAGCAATCGTGTCTTGGCAATCTGTGAGGGGCCAGCTATTAAGAGTTCTTAGACAA 960
Db 901 CCATCAATCGTGTGTGCAATCCAGGTGAGGGTTCCAGTTATTAAGACTTCTCGACAA 960
Qy 961 GCAGAAATACAGGTCTCAAGACTGACTATCAAGATGCGATCTTCATCACCCTACA 1020
Db 961 GAAAGAAACCGAGCTTACACACTGAGCTATCTAATGCGATCTTCGTCACCTCAC 1020
Qy 1021 GCCCCCTCTATCAAGAGAGCACACAGGCAAGCAACGGGCAATCAGAGCG 1077
Db 1021 GCCCCCTCTATCAAGAGACACACAGGATTTGCCAAAGTAGAGCAATGCTCAGC 1077

RESULT 10
US-08-838-151A-48
Sequence 48, Application US/08838151A
Publication No. US20010011379A1
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Lau, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838, 151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Geminivirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-48

Query Match 63.8%; Score 691.2; DB 8; Length 1062;
Best Local Similarity 78.4%; Pred. No. 6.6e-203;
Matches 828; Conservative 0; Mismatches 228; Indels 0; Gaps 0;

Qy 1 ATGCCCCCAAGAAATTTAGATTGATCAAGAACTATTCTTAATATCCCCAG 60
Db 1 ATGCCCCCAAGCTCAAAATTTAGATTGATCAAGAACTATTCTTAATATCCCCAG 60
Qy 61 TGCCTCTATCTAAGAAAGAGCACTTCCCAATTACAAACCTTAATACCCAGTCAAC 120
Db 61 TGCCTCTATCTAAGAAAGAGAGTTCTTCCCACTTCAAGAAATTCATCAGCCAGAA 120
Qy 121 AAGAAATTCATCAAAATTTGAGAGAGCTTCATGAAAATGGGAACTCATCTCATGTG 180
Db 121 AAAAAATTCATCAAAAGCTGTGAGGAACTGACAGAAATGGTGAACCTCATCTTCAATGCG 180
Qy 181 CTGTGAGTTGAAAGGATGATCAATGACGAATACAGATTCTTCAGCTGTCC 240
Db 181 CTGTGAGTTGAAAGGATGATGCTGCACAAAATTAAGATTTGTCAGCTGTATCC 240
Qy 241 CCAACCCGATCAGACATTTTCATCGAATATTCAGGAGCTTAATAGAGCTCGACGTC 300
Db 241 TCAACCAAGTTCAGACCTTTTCATCCGAACTTCAGGAGCTTAATAGAGCTCGACGTC 300
Qy 301 AATATCATATCCGACAAAGAGAGATACAAATGGAATGGGAGATTTCCAAATCGAGCGC 360
Db 301 AAGGATATCATCGACAAAGATGAGTCAATCGAATGGGAGCAATTCGAAATCGAGCGC 360
Qy 361 AGATCTGCAAGAGAGGCGAGAGTGTGATGATCATATGATGCGAAGCAATTAATGCA 420
Db 361 AGATCTGCAAGAGAGAGTGTGAGTGTGCAAGATGATGATGCGAAGCAATTAATGCA 420
Qy 421 GGTTCGTTCAATCTGCTTACGCGTTCTAAGGAGAGAACCCAAAGATTTGTATTA 480
Db 421 GATTCATATGATCTGCTTACGCGTTCTAAGGAGAGAACCCAAAGATTTGTATTA 480
Qy 481 CAAATCATATATCCGCTCTAATCTGAAGCAATATTCGCAAAAGGCTCCGGAACCGTGG 540
Db 481 CAAATCATATATCCGCTCTAATCTGAAGCAATATTCGCAAAAGGCTCCGGAACCGTGG 540
Qy 541 GTTCCTCATTTCAAGTCTCTTTCACTAAGCTTCTGACAGAGATGAGGAGCG 600
Db 541 GTTCCTCATTTCCGTTGTATCATCTAATGATTTCCGTTGTATGCAAGATGGGTT 600
Qy 601 GATTAATTAATTTGAGAGCGGTGACGCTGCGCCGCGGATGAGCTGATGATCATGTC 660
Db 601 GATTAATTAATTTGAGAGCGGTGACGCTGCGCCGCGGATGAGCTGATGATCATGTC 660
Qy 661 GAGGTATTCAGAAACAGGAGAGAGATGAGGCGGTGAGGCGGACCAATATAT 720
Db 661 GAGGTATTCAGAAACAGGAGAGAGATGAGGCGGTGAGGCGGACCAATATAT 720
Qy 721 CTCAGTGAACCTAGACTTCAATGATGAGTCTTCTGATGATGAGCAATTAAGCTG 780
Db 721 TTTAGCGGTCTATTTGAGCTTAAATTCAGTGTCTATTCAGAGAGTGAATCAAGCTG 780
Qy 781 ATTGATGATCGACCGCATTTATTAAGCTTAAGCACTGAAAGATTTGCTGGGCGC 840
Db 781 ATTGATGATCGACCGCATTTATTAAGCTTAAAGCACTGAAAGATTTGCTGGGCGC 840
Qy 841 CAGAAATTTGGCAATGAATTTGCAATGAGTGAAGCAATTAAGAGGCGGATC 900
Db 841 CAAAGAGCTGGCAATTTAATCTGAATTAAGGAAAGCGGTTCAATTAAGAGGAGATA 900
Qy 901 CCAGCAATCGTGTCTTGGCAATCTGTGAGGGGCCAGCTATTAAGAGTTCTTAGACAA 960
Db 901 CCATCAATCGTGTGTGCAATCCAGGTGAGGGTTCCAGTTATTAAGACTTCTCGACAA 960
Qy 961 GCAGAAATACAGGTCTCAAGAACTGACTATCAAGATGCGATCTTCATCACCCTACA 1020
Db 961 GAAAGAAACCGAGCTTACACACTGAGCTATCTAATGCGATCTTCGTCACCTCAC 1020
Qy 1021 GCCCCCTCTATCAAGAGAGCACACAGGCAAGCTTA 1056
Db 1021 GCCCCCTCTATCAAGAGACACACAGGATTTGCCAA 1056

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RESULT 11
US-08-838-151A-51
; Sequence 51, Application US/08838151A
; Publication No. US20010011379A1
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bean Golden Mosaic Geminiivirus
; STRAIN: Type II
; INDIVIDUAL ISOLATE: Guatemala
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1059
; US-08-838-151A-51

Query Match 63.8%; Score 691.2; DB 8; Length 1062;
Best Local Similarity 78.4%; Pred. No. 6,6e-203;
Matches 828; Conservative 0; Mismatches 228; Indels 0; Gaps 0;

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Db 181 CTTATTCAATTCGAAGTAATTCCTGTCACAAATTAAGATTGTCGACTGATCC 240
Qy 241 CCAACCCGGTCAGACATTTCCATCCGAATATTGAGGAGCTAAATCGAGCTCGAGTC 300
Db 241 TCAACGAGGTGACGACCTTTCCATCCGAATATTGAGGAGCTAAATCGAGCTCGAGTC 300
Qy 301 AATTCATCATCGACAGAGCGAGATTAATGAAATGGGAGATTTCCAAATCGAGCGC 360
Db 301 AAGCATATACATCAACAAAGATGAGATCGAATCGAATGGGAGCAATTCGAAGTCAGCGC 360
Qy 361 AGATCTGCGAGAGGAGGAGCGAGCTGCTAATGATTAATGATCGAATGCAATTAATGCA 420
Db 361 AGATCTGCGAGAGGAGGAGCTGCTAATGATTAATGATCGAATGCAATTAATGCA 420
Qy 421 GGTTCGTTCAATCTGCTGCTTCACTAAGGATTCGAAGGAGAAACAACAAAGATTTGATTA 480
Db 421 GATTCATTAATGATCTGCTGCTTCACTAAGGATTCGAAGGAGAAACAACAAAGATTTGATTA 480
Qy 481 CAAATCATTAATCTGCTGCTTCACTAAGGATTCGAAGGATTCGAAGGATTCGAAGGATTCGA 540
Db 481 CAAATCATTAATCTGCTGCTTCACTAAGGATTCGAAGGATTCGAAGGATTCGAAGGATTCGA 540
Qy 541 GTTCCCTCAATTCGAAGTCTGCTTCACTAAGGATTCGAAGGATTCGAAGGATTCGAAGGATTCGA 600
Db 541 GTTCCCTCAATTCGAAGTCTGCTTCACTAAGGATTCGAAGGATTCGAAGGATTCGAAGGATTCGA 600
Qy 601 GATTAATTAATTCGAGGAGCGGTCGAGCTGCGCGCGCGAGATAGACCTGTAAGTATCATCTGC 660
Db 601 GACGACTAATTCGAGGAGCGGTCGAGCTGCGCGCGCGAGATAGACCTGTAAGTATCATCTGC 660
Qy 661 GAGGTCGATTCAGAAACAGGAGAAAGATGTCGCGCGCGAGATAGACCTGTAAGTATCATCTGC 720
Db 661 GAGGTCGATTCAGAAACAGGAGAAAGATGTCGCGCGCGAGATAGACCTGTAAGTATCATCTGC 720
Qy 721 CTGAGTGAACACCTGATCACTTCAATGTCGAGTCTTCGATGATGTCAGTATTAACGTC 780
Db 721 TTGAGCGGTTCATTTGACCTTTAATTCACGTCGTATTCACGCAAGTGAATCAACGTC 780
Qy 781 ATTGATGACATGCGACCGGATTAATCTAAGCTTAAGCACTGGAAGATTCGCGGCGC 840
Db 781 ATTGATGACATGCGACCGGATTAATCTAAGCTTAAGCACTGGAAGATTCGCGGCGC 840
Qy 841 CAGAAAGATTCGCAATCAATTCAGATGACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 900
Db 841 CAGAAAGATTCGCAATCAATTCAGATGACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 900
Qy 901 CAAAGGACTGGCAATCTAATCTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 960
Db 901 CAAAGGACTGGCAATCTAATCTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 960
Qy 961 GCAGAAATATCAGGTCCTCAAGAACTGACTATCAAGATGCGATCTTCATCACTGACCTGACA 1020
Db 961 GAGGAAATATCAGGTCCTCAAGAACTGACTATCAAGATGCGATCTTCATCACTGACCTGACA 1020
Qy 1021 GCGCCCTCTATCAAGAGACGACACGAGCAAGCCAA 1056
Db 1021 GCGCCCTCTATCAAGAGACGACACGAGCAAGCCAA 1056

RESULT 12
US-08-838-151A-54
; Sequence 54, Application US/08838151A
; Publication No. US20010011379A1
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:

```

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ADDRESS: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Geminivirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-54

Query Match      63.7%; Score 689.6; DB 8; Length 1062;
Best Local Similarity 78.3%; Pred. No. 2.1e-202;
Matches 827; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

QY 1 ATGCCCCCAACCAAGAAATTAGAGTTCAGTCAAGAACTATTCCATCTATCCCGAG 60
DB 1 ATGCCCAACCTCAAGATTAGAGTTCAGTCAAGAACTATTCCATCTATCTCTGT 60
QY 61 TGTCTCTATCTAAGAAAGACACTTCCCAATTACAAAACCTAAATACCCAGTCAC 120
DB 61 TGCCCTATACCGAAGAAAGAGTTCTTTCGCACTTCAGAAAGATTCAATACAGCCAGAT 120
QY 121 AAGAAATTCATCAAAATTTGCAAGAGCTTATGAAAAATGGGGAACCTCATCTCCATGTG 180
DB 121 AAAAAATTCATCAAAAGTCTGTGAGGAACTGCACAGAAATGTGAACTCATCTTCATGCG 180
QY 181 CTGTTCAGTTCGAAGGTAAGTACCAATGACGAATAACAGATTCTTCGACCTGCTGCC 240
DB 181 CTATTCAATTCGAAGGTAATGCTGTGCACAAATTAAGATTTGCTGACCTGATATCC 240
QY 241 CCAACCCGGTCAGACATTTTCATCCGAATATTCAGGAGCTAAATCGAGCTCGACGTC 300
DB 241 TCAACCAAGTCAAGACCTTTTCATCCGAACATTCAGGAGCTAAATCAAGTTGAGAGCTC 300
QY 301 AAATCATACATCCGACAGAGAGGATACATTCGAATGGGGAGATTTCCAAATGAGCGC 360
DB 301 AAGGCATACATCCGACAAAGATGAGTCAATTCGAATGGGGAACAATTCGAAGTGAAGCGC 360
QY 361 AGATTCGCGAGAGAGGCGAGAGCTGCTAATGATTCAATTCGGAAGAGCAATTAATGCA 420
DB 361 AGATTCGCAAGAGAGGTCAGCAAGTCTGCGCAACGATCTATATGGAAGGCAATTAAGCA 420
QY 421 GGTTCGGTCAATCTGCTTAGCGTTCTAAGGAGAACCAACCAAGATTTGTATTA 480

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DB 421 GATTCAATGATATGCTTGGACATATTTGAAGGAAACACCGAAGATTAGTCTT 480
QY 481 CAAATATATAATCCGCTCTTAACCTAGAACAAATATTCGCAAAAGCTCCGGAACGCTGG 540
DB 481 CAACATCAACAATCCCTTCTTAATCTCGAAACGATCTTCATCAAAAGCCGGAACCAATGG 540
QY 541 GTTCCTCATTTCAAGCTCTCTTTTCACTAAGTCTGACAGAGATGAGAAATGGGCG 600
DB 541 GTTCCTCATTTTCCGTTGTATCATTTATCAATGTTCCGTTGTTATTCAGAAATGGGTT 600
QY 601 GATTAATATTTCGAGACGGGTGACGCTGCGCCGCGGATAGACCTGTAAGTATCATGTC 660
DB 601 GAGACATATTTCGGAAGGGGTCCGCTGCCGCGGGAAGAACTTATTAATCATGCTC 660
QY 661 GAGGTATTTCAAGAACAGGAGAACGATGTGGCGGCTGCTTAAGGCCCAATTAAT 720
DB 661 GAAGGTATTTCAAGAACCGGAAGAACAAATGTGGCTGCTCATTAAGACACATTAAT 720
QY 721 CTCAGTGACACCTAGACTTCAATGTCAGTCTTCTCGAATGATGTCAGTAAAGCTG 780
DB 721 TTGAGCGGTCAATTTGACCTTAATTCACGTGTCTAATTCACGAGTGAATACAGCTC 780
QY 781 ATTGATGACATCGGACCGCATTTATCTAAGCTAAAGCATGGAAGAAATTGCTGGGGCC 840
DB 781 ATTAGAGACATTAAGCCCAATTTATTGAAGTAAAGCATGGAAGAACTAATTTGGGGCA 840
QY 841 CAGAAAGATTGGCAATTAATTTGCAAGTACGTAAAGCAATTCATAATTAAGGCGGATC 900
DB 841 CAAAGGACCTGGCAATTAATCTGAATATGAAAGGCGGTTCATAATTAAGGAGATA 900
QY 901 CCAAGCATCGTCTTTCATCTGTCAGTGGTGCAGCTATTAAGAGTTCTTATAGACAA 960
DB 901 CCAATCATCGTGTGTTCATCTGTCAGTGGTGCAGTGTTCATTAAGAGTTCTTATAGACAA 960
QY 961 GCAGAAATACAGGTCTCAAGAACTGACATATCAAGATCGATCTTCAATCACCCTACA 1020
DB 961 GAAGAAACCGAGCTTACACAACTGACATATCATATGATCGATCTTCAATCACCCTACA 1020
QY 1021 GCCCCTCTATCAAGAGACACACAGGCAAGCCAA 1056
DB 1021 GCCCCTCTATCAAGACACACAGGATTTGCCAA 1056

RESULT 13
US-10-633-850-79
Sequence 79, Application US/10633850
Publication No. US20040205843A1
GENERAL INFORMATION:
APPLICANT: Hanley-Bowdoin, Linda
APPLICANT: Orozco, Beverly M.
APPLICANT: Griseem, Wilhelm
TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
FILE REFERENCE: 5051.4581P
CURRENT APPLICATION NUMBER: US/10/633,850
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 09/289,346
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 60/125,004
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patent version 3.2
SEQ ID NO 79
LENGTH: 1056
TYPE: DNA
ORGANISM: Tomato golden mosaic virus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1056)
OTHER INFORMATION: TGMV AL1 KI44 mutant
US-10-633-850-79

Query Match      56.1%; Score 607.4; DB 18; Length 1056;

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Best Local Similarity 73.7%; Pred. No. 6e-177;
Matches 773; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

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QY 5 CCCACCAAGAAATTGAGTTCAGTCAAGAACTATTTCTTAATTATCCCAAGTCT 64
DB 8 CGCATCCAAAACGGTTCAATATAATGCAAAAATTTTCTTACATATCCTCAGTCT 67
QY 65 CTCTATTTAAAGAAAGCACTTTCCCAATTAACAAAATTAATATCCCAAGTCAAGA 124
DB 68 CCTGTGCAAGAAAGTCACTTTCTCAATTAACAAGCCCTAAACACCTCGATTAAACAAA 127
QY 125 AATTCAATCAAAATTTGAGAGCTTCATGAAAATGGGAAACCTCATCTCCATGCTTG 184
DB 128 AATTCAATCAAAATTTGAGAGCTTCATGAAAATGGGAAACCTCATCTCCATGCTTG 187
QY 185 TTGAGTTGAGAGTAACTACCAATGACAGATTAACAGATTTCTTGACCTGCTCCCAA 244
DB 188 TTGAGTTGAGAGTAACTACCAATGACAGATTTCTTGACCTGCTCCCAA 247
QY 245 CCGGTCAGACATTTCCATCCGAAATTCAGAGGAGTAAATGAGCTCCGAGCTCAAT 304
DB 248 CAAGTCAGACATTTCCATCCGAAATTCAGAGGAGTAAATGAGCTCCGAGCTCAAG 307
QY 305 CATACATCGACAAGAGAGGATACATTCGAAATGGGAGATTTCCAAATGAGCGGAGAT 364
DB 308 CATACATCGACAAGAGAGATACATTCGAAATGGGAGATTTCCAAATGAGCGGAGAT 367
QY 365 CTGCGAGAGAGGCGACAGTCTGCTATGATTAATGCGAAAGATTAATGAGGAT 424
DB 368 GTGCTGAGAGAGGTTGCGAAACATCTAACGAGCTGAGAGAGGCTTAAATGCTTCT 427
QY 425 CGGTTCAATCTGCTTACCGGTTCTAAGGAAACCAACCAAGATTTGTATTACAA 484
DB 428 CCGGAGAGAGGCTGCTGAGATTAAGAGAAATCCCAAGAAATATTATTATTCAGT 487
QY 485 ATCAATACATCCGCTTAACCTGAGAAAGAAATTCGAAAGGCTCGGAAACCGGAGT 544
DB 488 TCACATCTTAATGAAATTAAGATTAAGATTAAGATTCGAAAGGCTCGGAAACCGGAGT 547
QY 545 CTCATTTCAAGTCTCTTCTTCACTAACGTTCTCTGAGAGATGAGAGATGGGCGATA 604
DB 548 CTCGTTTCAAGTCTCTTCTTCACTAACGTTCTCTGAGAGATGAGAGATGGGCGATA 607
QY 605 ATTAATTTGGGAGCGGAGTCTGCGGCGGCGGATGAGCTGTAATGATCATGCTGAG 664
DB 608 ATTAATTTGGGAGCGGAGTCTGCGGCGGCGGATGAGCTGTAATGATCATGCTGAG 667
QY 665 GTGATTCAGAAAGAGGAGAGGATGAGGAGGCGGCTGTAATGAGGCGGATGATCA 724
DB 668 GTGATTCAGAAAGAGGAGAGGATGAGGAGGCGGCTGTAATGAGGCGGATGATGGA 727
QY 725 GTGAGACCTAGACTTCAATGAGTCTTCTGAAATGATGAGTATTAACGTCATG 784
DB 728 GTGAGACCTAGACTTCAATGAGTCTTCTGAAATGATGAGTATTAACGTCATG 787
QY 785 ATGACATCGACCGGATTTATCTAAAGCTAAAGCACTGAGAAAGATGCTGGGCGGAGA 844
DB 788 ATGACATCGACCGGATTTATCTAAAGCTAAAGCACTGAGAAAGATGCTGGGCGGAGA 847
QY 845 AAGATTGGCAATCAAAATTTGAGAGGATGAGGAGGCTGTAATTAAGGAGGAAATCCAG 904
DB 848 AAGATTGGCAATCAAAATTTGAGAGGATGAGGAGGCTGTAATTAAGGAGGAAATCCAG 907
QY 905 CAATGCTGCTTGTGCAATCTGAGAGGAGTCAAGCTTAAGAGATTTAGACAAAGCAG 964
DB 908 CAATGCTGCTGCTGCAATCTGAGAGGAGTCAAGCTTAAGAGATTTAGACAAAGCAG 967
QY 965 AAAATACAGGCTTCAAGAACTGAGCTATCAAGATGAGATTTATCACTCAGAGCC 1024
DB 968 AAAATACAGGCTTCAAGAACTGAGCTTATCAAGATGAGAAATGCTCCTCAATCCC 1027
QY 1025 CCTCTATCAAGAGAGCAGAGCAAGC 1053
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DB 1028 CCTCTATCAAGAGCTCAACAGAGCAGC 1056

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RESULT 14
US-10-633-850-83
; Sequence 83. Application US/10633850
; Publication No. US20040205843A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Griseem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.4581P
; CURRENT APPLICATION NUMBER: US/10/633,850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
; LENGTH: 1056
; TYPE: DNA
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1056)
; OTHER INFORMATION: TMV AL1 E146 mutant
US-10-633-850-83
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Query Match 56.1%; Score 607.4; DB 18; Length 1056;
Best Local Similarity 73.7%; Pred. No. 6e-177;
Matches 773; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

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QY 5 CCCACCAAGAAATTGAGTTCAGTCAAGAACTATTTCTTAATTATCCCAAGTCT 64
DB 8 CGCATCCAAAACGGTTCAATATAATGCAAAAATTTTCTTACATATCCTCAGTCT 67
QY 65 CTCTATTTAAAGAAAGCACTTTCCCAATTAACAAAATTAATATCCCAAGTCAAGA 124
DB 68 CCTGTGCAAGAAAGTCACTTTCTCAATTAACAAGCCCTAAACACCTCGATTAAACAAA 127
QY 125 AATTCAATCAAAATTTGAGAGCTTCATGAAAATGGGAAACCTCATCTCAGTGTG 184
DB 128 AATTCAATCAAAATTTGAGAGCTTCATGAAAATGGGAAACCTCATCTCAGTGTG 187
QY 185 TTGAGTTGAGAGTAACTACCAATGACAGATTAACAGATTTCTTGACCTGCTCCCAA 244
DB 188 TTGAGTTGAGAGTAACTACCAATGACAGATTAACAGATTTCTTGACCTGCTCCCAA 247
QY 245 CCGGTCAGACATTTCCATCCGAAATTCAGAGGAGTAAATGAGCTCCGAGCTCAAT 304
DB 248 CAAGTCAGACATTTCCATCCGAAATTCAGAGGAGTAAATGAGCTCCGAGCTCAAG 307
QY 305 CATACATCGACAAGAGAGGATACATTCGAAAGGCTCGGAAATTAATGAGGAGAT 364
DB 308 CATACATCGACAAGAGAGGATACATTCGAAAGGCTCGGAAATTAATGAGGAGAT 367
QY 365 CTGCGAGAGAGGCGACAGTCTGCTATGATTAATGAGGAGGCTTAAATGAGGAT 424
DB 368 GTGCTGAGAGAGGTTGCGAAACATCTAACGAGCTGAGAGAGGCTTAAATGAGGAT 427
QY 425 CCGTTCATCTGCTTGTGCAATCTGAGAGGATGAGGAGGCTTAAATGAGGAT 484
DB 428 CCAAGAGAGAGGCTGAGAGATTAATGAGAGGAGGATTAATTAATTTTCACT 487
QY 485 ATCAATACATCCGCTTAACTGAGAAAGATTAATGAGGAGGCTCCGAAACGCTGCT 544
DB 488 TCACATCTTAATGAAATTAAGATTAAGATTAAGATTCGAAACGATGCTTC 547
QY 545 CTCATTTCAAGGCTGCTTCTTCACTAAGCTTCGAGAGGATGAGGAGGAGATA 604
```

Dh 548 CTCGGTCCAGCTCATCTATCTACTAAGCGCCAGAGAGATGAGCAATGGGCTGAAA 607
Qy 605 ATATATTCGGGAGCGGGTGAAGCGTCCGCCGAGTAAAGCTGTAAATCATCTGCGAGG 664
Dh 608 ATATATTTGGAAAAGTTCCGCTGGCGGCGGAGAGACCTATTAGTAATCATCTGAGG 667
Qy 665 GTGATTCAGAAACAGGAGAGAGATGTGGGCGCTGGGTTAGGCCCATTAATCATCTCA 724
Dh 668 GCGATTAATCGGACGGGAAAAGATATGTGGGCTCGTTACATAGGCCCATTAATTTTGA 727
Qy 725 GTGACACCTAGACTTCAATGTGCGAGCTTTCTGAAATGATGTGAGATTAACGTCAATG 784
Dh 728 GCGGGCATTTGGATCTCAATTTCTAGGGTTTAACTCAAAAGGTTAGATTAACGTCAATG 787
Qy 785 ATGACATCGCACCGGCATTTATTTAAGCTTAAGCATCTGAAAAGAAATGTGGGGGCCA 844
Dh 788 ATGATGTACACCGCAATATCTTAAGTTGAAACATTTGAAAGAACTAATGGGGCCCAA 847
Qy 845 AAGATTGGCAATCAAAATTTGCAAGTACGTTAAGCCAGTTCAAAATTAAGCGGAATCCAG 904
Dh 848 GAGATTGGCAGACTTAATCTGTAAATACGAAAGCCAGTTCAAAATTAAGAGATATCCCGT 907
Qy 905 CAATCGTCTTTTGAATCTGTGTAGGGGTGCGACCTTAATAAGCTTTAGACAAAGCAG 964
Dh 908 CAATCGTGTGTGCAATCTGTAGAGAGGGTGTACTAATAAGTTTCTCGACAAAGAGG 967
Qy 965 AAAATACAGGTCTCAAAATCTGACCTATCAAGAAATGGATCTTATCACTCAAGCCC 1024
Dh 968 AAAACACTCCACTTAAGAAACCTGACTTTCATTAATGGAAATGCTTCTCTCAACTCCC 1027
Qy 1025 CCCTCTATCAAGAGACACAGGCAAGC 1053
Dh 1028 CCCTCTATCAAAAGCTCAACACAGAGCAGC 1056

RESULT 15
US-10-633-850-50
; Sequence 50, Application US/10633850
; Publication No. US20040205843A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Grubisem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.4581P
; CURRENT APPLICATION NUMBER: US/10/633,850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 1056
; TYPE: DNA
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1056)
; OTHER INFORMATION: TGMV AL1 coding sequence
US-10-633-850-50

Query Match 55.9%; Score 605.8; DB 18; Length 1056;
Best Local Similarity 73.6%; Pred. No. 1.9e-116;
Matches 772; Conservative 0; Mismatches 277; Indels 0; Gaps 0;

Qy 5 CCCACCAAGAAATTTAGATTGAGTTCAGTCAAGAACTATTTCTTACTTATCCAGAGCT 64
Dh 8 CGCATCCAAACGCTTCAATATAATGCCAAAATTTATTTCTTACATATCTCAGTGCT 67
Qy 65 CTCTATTAAGAAGAAAGACTTTCCCAATTACAAAACCTAAATACCCAGTCAACAGA 124

Dh 68 CTTGTCCAAAGAAATCACTTTCTCTCAATTAAGAGCCCTAAACACTCCGATTAACAAAA 127
Qy 125 AATTCATCAAAATTTGAGAGAGCTTATGAAAATGGGAAACCTCATCTCCATGTGTTG 184
Dh 128 AATTCATCAAAATTTGAGAGAGCTTATGAAAATGGGAAACCTCATCTCCATGTGTTA 187
Qy 185 TTGAGTTCAAGAGTTAAGTACCAATGACAGATTAACAGATTTCTTCACTGGTCTCCCAA 244
Dh 188 TTGAGTTCAAGAGAAATATGCTGTCGCAAAATCAAGATTTCTTCACTGGTCTCCCAA 247
Qy 245 CCGGTCAGACATTTTCATTCGAAATTTGAGGAGCTTAATGAGCTCCGAGCTCAAT 304
Dh 248 CAAGGTGAGACATTTTCATTCGAAACATTCAGAGAGCTTAATGAGCTCCGAGCTCAAG 307
Qy 305 CATATTCGACAAAGAGAGGATATCAATCGAATGGGAGATTTCCAAATGAGAGCGAGAT 364
Dh 308 CGTACATCGACAAAGAGAGGATATCTTGTATGGGAGAAATTCAGAGTGAAGCGGTGAA 367
Qy 365 CTGCGAGAGAGGCGACAGCTGTGTTATGATTCATATGCGAAAGCATTAATGCAAGTT 424
Dh 368 GTGTAAGAGAGGTTGCGCAACATCTTAACAGAGCTGACAGAGAGCGTTAAATGCTTCT 427
Qy 425 CGGTTCAATCTGCTTAGCGGTTCTTAAGGAGAAACCAAAAAGATTTGTATTAACAA 484
Dh 428 CCAAGAGAAAGCCCTGACAGATTAATGAGAGAAATCCAGAAAATATTTATTTAGT 487
Qy 485 ATATATCATCCGCTTAACCTTAAGAGAAATTTGCGAAAGGCTCCGGAACCGGGGCTC 544
Dh 488 TCACAAATCTTAATAGCAATTTAGATGATTTGATTAAGATCTCGAACCATGAGCTTC 547
Qy 545 CTCATTTCAAGTCTCTTTCTTCACTAACCTTCTGACGAGATGAGAAATGGGCGGATA 604
Dh 548 CTCGGTTCCAGTCTCTATCATTTAATCTTAACGTGCGACAGAGATGAGCAATGGGCTGAA 607
Qy 605 ATATATTCGGAAGGAGTGAAGCTGCGCGCGCGGATAGACTGTATGATCATGTGAGG 664
Dh 608 ATATATTTGAAAAGAGTTCGCTGCGCGCGGAGAGACCTATTAATGATCATGAGG 667
Qy 665 GTGATTCAGAAACAGGAGAGAGATGTGGGCGGTGATTAAGGCCCATTAATGATCTCA 724
Dh 668 GCGATTAATCGAGGAGGAAAGATATGTGGGCTGTGTACTAAGGCCCATTAATTTTGA 727
Qy 725 GTGACACCTAGACTTCAATGATGTGAGTCTTTCGAATGATGTGACATTAACGTCAATG 784
Dh 728 GCGGCAATTTGATCTCAATTTCTAGGTTTACTCAAAACAAGTTGATTAACGTCAATG 787
Qy 785 ATGACATCGCACCGCATTTATCTTAAGCTTAAGCATGGAAGAAATGCTGGGGCCAGA 844
Dh 788 ATGATGTACACCGCATATCTTAAGTTGAAACATTTGGAAGAACTCATTTGGGGCCCAA 847
Qy 845 AAGATTGGCAATCAAAATTTGCAAGTACGTTCAAGCTTAATAAGGGGGAATCCAG 904
Dh 848 GAGATTGGCAGACTTAATCTGTAAATACGAAAGCCAGTTCAAAATTAAGAGATATCCCGT 907
Qy 905 CAATCGTCTTTTGAATCTGTGTAGGGGTGCGACCTTAATAAGGTTCTTGAAGAGCAG 964
Dh 908 CAATCGTGTGTGCAATCTGTAGAGGGGTCTAGCTATAAAGTTTCTCGACAAAGAGG 967
Qy 965 AAAATACAGGTCTCAAGAACTGAGATCTAAGAAATGGATCTTCAATCACTCAAGCCC 1024
Dh 968 AAAACACTCCACTTAAGAAACCTGACTTTCATTAATGGAATTCGTTCTCTCAACTCCC 1027
Qy 1025 CCCTCTATCAAGAGACACAGGCAAGC 1053
Dh 1028 CCCTCTATCAAGCTCAACACAGAGCAGC 1056

Search completed: December 4, 2004, 17:49:13
Job time : 633 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2004, 13:14:20 ; Search time 3903 Seconds

(without alignments)
1011.255 Million cell updates/sec

Title: US-09-491-063a-1

Perfect score: 1083

Sequence: 1 atgcccccccaagaalt.....gcaatcagaagcgacgggt 1083

Scoring table: IDENTITY NUC

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	47.2	4.4	636	B2394806	B2394806 EINB009TF
C 2	43.2	4.0	977	CNS0405K	AL266481 Tetradon
C 3	41.8	3.9	791	C0088898	CO088898 GR_Ea08B
C 4	41	3.8	864	AO891340	AO891340 HS_3143_A
C 5	40.8	3.8	822	CNS011PO	AL100566 Drosophi1
C 6	40.4	3.7	609	BM370082	BM370082 BM370082
C 7	40.4	3.7	665	AV957294	AV957294 AV957294
C 8	40.4	3.7	697	CNS018M5	AL109511 Drosophi1
C 9	39.8	3.7	607	BP764040	BP764040 BP764040
C 10	39.8	3.7	739	BX262586	BX262586 BX262586
C 11	39.6	3.7	2433	CNS0A7F8	BX823253 Arabidops
C 12	39.6	3.6	738	BX200121	BX200121 Dario rer
C 13	39.4	3.6	762	CC375636	CC375636 PUM234TB
C 14	39.4	3.6	933	B2826521	B2826521 PUGC1.7TD
C 15	39.4	3.6	945	C0168857	CG168857 PUFROV4TB
C 16	38.6	3.6	640	AO254323	AO254323 CP60765B
C 17	38.6	3.6	1102	CNS01521	AL104916 Drosophi1
C 18	38.4	3.5	1310	CNS0152M	AL106118 Drosophi1
C 19	38.2	3.5	700	BUR25743	BUR25743 603742692
C 20	38	3.5	615	BM300507	BM300507 MCA053B12
C 21	38	3.5	723	CL593149	CL593149 OB_Ba005
C 22	38	3.5	849	CC504462	CC504462 CH240_344
C 23	38	3.5	911	CC092222	CC092222 CSU-K34.1
C 24	38	3.5	939	CNS00CNG	AL059400 Drosophi1

25	37.6	3.5	784	5	BUR26709	BUR26709 603610148
26	37.6	3.5	1145	7	CK161861	CK161861 PAS01443
C 27	37.4	3.5	477	5	BY249188	BY249188 BY249188
28	37.4	3.5	546	5	BP033725	BP033725 BP033725
29	36.6	3.4	713	5	BU443152	BU443152 604144395
C 30	36.6	3.4	740	5	CC120153	CC120153 NDL_73M13
C 31	36.6	3.4	783	9	BX145514	BX145514 Dario rer
C 32	36.6	3.4	854	8	B21413	B21413 T14124-5p6
C 33	36.4	3.4	535	9	CR313399	CR313399 Medicago
C 34	36.4	3.4	693	8	BZ07541	BZ07541 h59c08.b
C 35	36.4	3.4	818	6	CD439694	CD439694 E01N0527
C 36	36.4	3.4	829	9	CC919532	CC919532 t025a11b8
C 37	36.4	3.4	836	9	CG267577	CG267577 OXKCU71TH
38	36.4	3.4	920	9	CG197027	CG197027 PUFMO55TD
C 39	36.4	3.4	931	9	CG074022	CG074022 PUHO83TD
C 40	36.4	3.4	954	9	CG197026	CG197026 PUFMO55TB
C 41	36.2	3.3	445	8	CC054409	CC054409 SALK_0601
C 42	36.2	3.3	483	9	BX167127	BX167127 Dario rer
C 43	36.2	3.3	733	6	CA946230	CA946230 000271 BO
C 44	36.2	3.3	930	9	BX966641	BX966641 Forward 8
C 45	36.2	3.3	418	5	BU711438	BU711438 SJAAME09

ALIGNMENTS

RESULT 1
LOCUS B2394806/c 636 bp DNA linear GSS 30-APR-2003
DEFINITION EINB009TF EI_10_12_KB Entamoeba invadens genomic clone EINB009,
genomic survey sequence.
ACCESSION B2394806
VERSION B2394806.1 GI:30241347
KEYWORDS GSS.
SOURCE Entamoeba invadens
ORGANISM Entamoeba invadens
REFERENCE Wang,Z., Samuelson,J., Clark,C.G., Eichinger,D., Paul,J., van Dellen,K., Hall,N., Anderson,I. and Loftus,B.
Gene discovery in the Entamoeba invadens genome
Mol. Biochem. Parasitol. 129 (1), 23-31 (2003)
JOURNAL MEDLINE 22684048
PUBMED 12798503
COMMENT Other GSSs: EINB009TR
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
DNA was provided by Daniel Eichinger
Seg primer: TF
Class: sheared ends.
FEATURES
Location/Qualifiers
1..636
/organism="Entamoeba invadens"
/mol_type="genomic DNA"
/strain="TF-1"
/db_xref="taxon:33085"
/clone="EINB009"
/clone_1fb="EI_10_12_KB"
/note="Vector: pHO52; Site 1: Batx1; Total genomic DNA was isolated from early log phase trophozoites of E. invadens IP-1 using a Qiagen plant DNA extraction kit. A shotgun medium-size plasmid library (average insert size of 10 - 12 kb) was generated by random mechanical shearing of E. invadens genomic DNA, repairing the ends of DNA fragments with T4 Polymerase, adding Batx1 adaptors and ligating into the Batx1 site of a pUC-derived vector pHO52."

ORIGIN

Query Match 4.4%; Score 47.2; DB 8; Length 636;
 Best Local Similarity 50.4%; Pred. No. 0.015;
 Matches 115; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 12 AAAGAAATTAGAGTTCAGTCAAGAACTATTTCTTAAGTTATCCGAGTCTCTATC 71
 DB 284 AAACCTTCAGATTAAACGGAAGACCTGCTCTTAACATGCGACAGACACTCTCC 225
 QY 72 TAAAGAAAGACCTTCCCAATTAACAACCTAAATACCAGTCAACAGAAATTCAT 131
 DB 224 AAAAGAAAGACGATGAAGAACTGAGAACTTAACTGAGACTATGAAATTAATATAT 165
 QY 132 CAAATTTGAGAGAGCTTCATGAATGAGAACTCATCTCATGTGCTTGTTCAGTT 191
 DB 164 AGTCGTGTCAGAGAAAAACGAAAGAGGAGCTGATCTATCATGAGTGTATAGCT 105
 QY 192 CGAAGTAACTACCAATGACGAATTAACAGATTCTTGACCTGCTC 239
 DB 104 GGAAGAAAGATGATTTTCAGAGATCAGAGCTGCTGAATCTAAGCTC 57

RESULT 2

CNS0405K 977 bp DNA linear GSS 01-SEP-2000
 LOCUS Tetradon nigroviridis genome survey sequence T7 end of clone
 DEFINITION 071D12 of library G from Tetradon nigroviridis, genomic survey
 sequence.

ACCESSION AL268481.1 GI:7990330
 VERSION GSS; genome survey sequence.
 KEYWORDS Tetradon nigroviridis
 SOURCE Tetradon nigroviridis
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthopterygii; Acanthopterygii; Percomorphi; Tetraodontiformes;
 Tetraodontidae; Tetraodontidae; Tetradon.

REFERENCE

AUTHORS Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F.,
 Saurin, W., and Weissenbach, J.
 TITLE Estimate of human gene number provided by genome-wide analysis
 using Tetradon nigroviridis DNA sequence
 JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
 MEDLINE 20296633
 PUBMED 10835645

REFERENCE

AUTHORS Roest Crolius, H., Jaillon, O., Dasilva, C., Ozouf-Coatz, C.,
 Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,
 Saurin, W., Bernot, A., and Weissenbach, J.
 TITLE Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetradon nigroviridis
 JOURNAL Genome Res. 10 (7), 939-949 (2000)
 MEDLINE 20359837
 PUBMED 10899143

REFERENCE

AUTHORS 3 (bases 1 to 977)
 TITLE Genoscope.
 JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT This sequence is a single read and was generated as part of a large
 scale clone-end sequencing project of the Tetradon nigroviridis
 genome. For more information, please take a look at
 http://www.genoscope.cns.fr/Tetradon.

COMMENT

FEATURES

source
 1. 977
 /organism="Tetradon nigroviridis"
 /mol_type="genomic DNA"
 /db_xref="taxon:99883"
 /clone="071D12"
 /clone_1b="G"
 /note="Genoscope sequence ID : COB071DB06DP1-end : T7"

ORIGIN

Query Match 4.0%; Score 43.2; DB 9; Length 977;
 Best Local Similarity 57.4%; Pred. No. 0.27;
 Matches 78; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 97 CAAACCTAAATATCCAGTCAACAGAAATTCATCAAAATTTGACAGAGCTTCATGAA 156
 DB 485 CAAATCTAATTTCCCATTCAAATGATATGATTTATGTAACAGATTAATACA 426
 QY 157 AATGGGAACCTATCTTCATGTGCTTGTTCAGTTGAAGTAAATGCAATGCAAT 216
 DB 425 GCGTTGGAGAGCAAGCTCGATGATGATGATGATGATGATGATGATGATGATGAT 366
 QY 217 AACGATTCCTTGACC 232
 DB 365 GAGCTATTAATTCCTCC 350

RESULT 3

CO088898 791 bp mRNA linear EST 16-JUN-2004
 LOCUS GR_Ea08B20.r GR_Ea Gossypium raimondii cDNA clone GR_Ea08B20 3',
 DEFINITION mRNA sequence.

ACCESSION CO088898
 VERSION CO088898.1 GI:48779532
 KEYWORDS EST.
 SOURCE Gossypium raimondii
 ORGANISM Gossypium raimondii
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

REFERENCE

AUTHORS Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C.,
 Udall, J. A., Rapp, R. A., Wendel, J. F., Rao, K., Soderlund, C. and
 Wing, R. A.
 TITLE Global assembly of cotton ESTs
 JOURNAL Unpublished (2004)
 COMMENT Contact: Rod A. Wing
 Arizona Genomics Institute
 The University of Arizona
 Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: http://genome.arizona.edu
 plate: 08 row: B column: 20.

JOURNAL

FEATURES
 source
 1. 791
 /organism="Gossypium raimondii"
 /mol_type="mRNA"
 /db_xref="taxon:29730"
 /clone="GR_Ea08B20"
 /tissue_type="whole seedlings"
 /dev_stage="first true leaves"
 /lab_host="DH10B"
 /clone_1b="GR_Ea"
 /note="vector: PCMV.SPORT-6.1; Site 1: NotI; Site 2:
 EcoRV; Library made by Invitrogen with RNA supplied by
 Wendle lab. Directional cloned into NotI-EV. Colonies
 plated/picked by Agt. More glycerol clones held in -80."

FEATURES

Location/Qualifiers
 1. 791
 /organism="Gossypium raimondii"
 /mol_type="mRNA"
 /db_xref="taxon:29730"
 /clone="GR_Ea08B20"
 /tissue_type="whole seedlings"
 /dev_stage="first true leaves"
 /lab_host="DH10B"
 /clone_1b="GR_Ea"
 /note="vector: PCMV.SPORT-6.1; Site 1: NotI; Site 2:
 EcoRV; Library made by Invitrogen with RNA supplied by
 Wendle lab. Directional cloned into NotI-EV. Colonies
 plated/picked by Agt. More glycerol clones held in -80."

ORIGIN

Query Match 3.9%; Score 41.8; DB 7; Length 791;
 Best Local Similarity 51.9%; Pred. No. 0.68;
 Matches 94; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 847 GATTGCAATCAATTCAGTACGATGATGATGATGATGATGATGATGATGATGATGAT 906
 DB 651 GAGTGGGCAACAGGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 592
 QY 907 ATCGTCTTGGCAATCTCTGTGAGGATGATGATGATGATGATGATGATGATGATGAT 966
 DB 591 TTATATCTGTAACATCTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 532

QY 967 AATACAGCTCTCAAGAACTGACTATCAAGATGCAATCTTATCCACCTTCAGACGCC 1026
 DB 531 GTCAAGGCTCTGGGACCGGACAAATTAGATGCACTTATCAAGACTTACTTGTCC 472
 QY 1027 C 1027
 DB 471 C 471

RESULT 4
 A0891340/c
 LOCUS
 DEFINITION HS_3143_A1_C01_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3143 Col=1 Row=E, genomic survey

ACCESSION A0891340
 VERSION A0891340.1 GI:6347530
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 864)
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and Hood,L.
 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 99380589
 10449764

COMMENT
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallaceu.washington.edu
 Clones may be purchased from Research Genetics (info@reagen.com).
 BAC end Web Server: http://www.htsc.washington.edu
 Plate: 3143 row: E column: 1
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 864.

FEATURES
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 Location/Qualifiers
 1..864
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=3143 Col=1 Row=E"
 /sex="male"
 /clone_1lb="CIT Approved Human Genomic Sperm Library D"
 /note="Organ: sperm; Vector: pBelobAC11; BAC clones in E-Coli DH10B"

ORIGIN
 Query Match 3.8%; Score 41; DB 8; Length 864;
 Best Local Similarity 50.8%; Pred. No. 1.2;
 Matches 98; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 205 CAATGCAGAAATTAACAGATTCTTGAGCTGTCTCCCAACCGGTACGACATTTCCAT 264
 DB 590 CACTGATACAAAATGCAATCTTCATCTAGTATCCCAAAAGCCCTCTAATCTTCC 531
 QY 265 CCGAATATTCAGGAGGATTAATCGAGCTCCGACGCTCAATCATCATCGACAAGACGGA 324
 DB 530 TTGACTGTGAACGGGCTAGATTATCAATCTTATATATATCTCTTATTAGAGGC 471
 QY 325 GATACATCAATGAGGAGATTTTCAATCGACGCGAGATTCGACAGAGAGGCGACAG 384
 DB 470 TTATATTAACCTGTCTGAAGATGACTAGTAGCAGAGGTTTTCAGTAGAGGATTA 411
 QY 385 TCTGCTAATGATT 397

DB 410 TCAGCAAAACGTT 398

RESULT 5
 CNS011PO/c
 LOCUS
 DEFINITION CNS011PO 822 bp DNA linear GSS 26-JUL-1999
 Drosophila melanogaster genome survey sequence 17 end of BAC BACN06K06 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL100566
 VERSION AL100566.1 GI:5612177
 KEYWORDS GSS.
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 822)

REFERENCE
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

FEATURES
 source
 Location/Qualifiers
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 /db_xref="taxon:7227"
 /clone="BACN06K06"
 /clone_1lb="DrosBAC"
 /plasmid="pBelobAC11"
 /note="end : T7"

ORIGIN
 Query Match 3.8%; Score 40.8; DB 9; Length 822;
 Best Local Similarity 39.0%; Pred. No. 1.4;
 Matches 96; Conservative 29; Mismatches 121; Indels 0; Gaps 0;

QY 6 CCGACAAAGAAATTTAGAGTTGAGTCAAGCAAGACTATTCCTAATCCAGTGC 65
 DB 773 YCCCAAAAWAAATTCAAATTAACTYTTAACTATTCCTAATTCACCAATTTTA 714
 QY 66 TCTATCTAAAGAAAGAGCACTTCCCAATTACAAACCTAATACCCAGTCAACAGAA 125
 DB 713 AAMATTAAATBBSAATAATCCSATTAATTSSSATTAATCAABAATTAACGCAAAA 654
 QY 126 ATTATCAAAATTTGCAAGAGCTTCATGAAATGGGAACTCATCTCATGTCTGT 185
 DB 653 CMCACAAACAATTTCAAGCATTAATTAATSSATTAATSSATTAATSSATTAATSS 594
 QY 186 TCACTGCAAGTAAATCAATCAATGCAAGCAATTAACAGATCTTGAGCTGTCTCCCA 245
 DB 593 TAGCGTCAATSAANAAGSCCAAAASATSWATCAATSCAATCAATTAATSSMASMTS 534
 QY 246 CCGGTC 251
 DB 533 CASCCTC 528

RESULT 6
 BM370082/c
 LOCUS
 DEFINITION BM370082 609 bp mRNA linear EST 28-MAY-2004
 BM370082 Yutaka Satou unpublished cDNA library, mature adult whole animal cDNA interstitials cDNA clone c1m849d15 5', mRNA sequence.

ACCESSION	BWJ70082
VERSION	BWJ70082.1
KEYWORDS	GI:47785910
SOURCE	EST.
ORGANISM	Ciona intestinalis Ciona intestinalis Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona. 1 (bases 1 to 609) Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N. Expressed genes in Ciona intestinalis (2004) Unpublished (2004) Contact: Yutaka Satou Department of Zoology Kyoto University Sakyo-ku, Kyoto, Kyoto 606-8502, Japan Tel: 81-75-753-4095 Fax: 81-75-705-1113 Email: yutaka@ascidian.zool.kyoto-u.ac.jp. Location/Qualifiers
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
FEATURES	
source	1..609 /organism="Ciona intestinalis" /mol_type="mRNA" /db_xref="taxon:7719" /clone="cima849d15" /tissue_type="whole animal" /dev_stage="mature adult" /clone_id="Yutaka Satou unpublished cDNA library, mature adult whole animal"
ORIGIN	
Query Match	3.7%; Score 40.4; DB 5; Length 609;
Best Local Similarity	53.9%; Fred.No.1.7;
Matches	83; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
Oy	681 GAAGCAGATGCGGGCGGTTCGAGCCCATATCTCAGTGCACACTGACTT 740 Db 274 GAAGAATTGTTCAATGATCTTTACACAATGATCCCTGCAAGTGAAACACTT 215 Oy 741 CAATGCTGAGTCTTCTGAATGATGTCAGATTAAGTCAATGATGACATGCCACCGCA 800 Db 214 TAAAGTCGTGGTGTCTTAAACGATGGGGAGGTGCACCATATGCGAAGTTGCACACA 155 Oy 801 TTATCTAAGCTAAAGCAGCTGGAAGATTTGCTG 834 Db 154 TTATATGACCTAATAATATGCAATCGTTATG 121
RESULT 7	
AV957294/c	665 bp mRNA linear EST 14-MAR-2002
LOCUS	
DEFINITION	AV957294 Nori Satoh unpublished cDNA library, egg Ciona
ACCESSION	intestinalis cDNA clone cleg14g03 5', mRNA sequence.
VERSION	AV957294
KEYWORDS	AV957294.1 GI:19445593
SOURCE	EST.
ORGANISM	Ciona intestinalis Ciona intestinalis Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona. 1 (bases 1 to 665) Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T. Expressed genes in Ciona intestinalis Unpublished (2000) Contact: Nori Satoh Department of Zoology Kyoto University Sakyo-ku, Kyoto, Kyoto 606-8502, Japan Tel: 81-75-753-4081 Fax: 81-75-705-1113 Email: satoh@ascidian.zool.kyoto-u.ac.jp. Location/Qualifiers
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
FEATURES	
source	1..665 /organism="Ciona intestinalis"

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		/clone_id="Nori Satoh unpublished cDNA library, egg"	
ORIGIN			
Query Match	3.7%;	Score 40.4;	DB 1; Length 665;
Best Local Similarity	53.9%;	Pred. No. 1.7;	Gaps 0;
Matches	83;	Conservative 0;	Mismatches 71; Indels 0;
Dy	681 GAAGACGATGTGGCGCCGTGCCTTAAAGCCCCAATACTATCTCAAGTGACAATTACTTT	740	
Dd	198 GAGAATTTGTCATWGAITCCTTAACAAATGATATCCCTGCAAGTGAACGAACCTTT	139	
OY	741 CAATGTCGACTCTTCTCGAATATATGCGCATATPACTCAATGATGACATCGCACCCC	800	
Dd	138 TAAAGTCGTGGTTGTCTTAAACGATGGGGAGGCGACCATATGCGAAGTTGCCAAC	79	
OY	801 TTATCTAAGCTAAGCACTGAAAAGATTGCTG	834	
Dd	78 TTATATGAACTTAATAATATGCAATGCTTATG	45	
RESULT 8 CN5018MS/c	697 bp DNA linear GSS 26-JUL-1999		
LOCUS	Drosophila melanogaster genome survey sequence T7 end of BAC		
DEFINITION	BACNI4C07 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.		
ACCESSION	CNS018MS		
VERSION	AL109511.1 GI:5629815		
KEYWORDS	GSS.		
SOURCE ORGANISM	Drosophila melanogaster (fruit fly)		
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyridroidea; Drosophilidae; Drosophila. 1 (bases 1 to 697) Genoscope. Direct Submission Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CRP (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAcII.		
COMMENT	Location/Qualifiers		
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Matches	86;	Conservative 29;	Mismatches 105; Indels 0;
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Dd	620 AAATWWMTTMAAMAAMATTAABAAAAAATTTMAAAAAAAMMACATWTTYTWTTATDMA	561	
OY	72 TAAAGAAAGACGACTTTCCCAATTACAAACCTTAATRCCCCAGTCAACAGAAATTATC	131	

LOCUS	DEFINITION	LOCUS	DEFINITION
BP764040	607 bp mRNA EST 10-JUL-2004	BP764040	607 bp mRNA EST 10-JUL-2004
BP764040 mouse (C57BL/6) pancreatic islet library with recombination-based method Mue musculus CDNA clone m1c30074 3', mRNA sequence.		BP764040 mouse (C57BL/6) pancreatic islet library with recombination-based method Mue musculus CDNA clone m1c30074 3', mRNA sequence.	
BP764040		BP764040	
BP764040.1 GI:50222738		BP764040.1 GI:50222738	
EST.		EST.	
Mus musculus (house mouse)		Mus musculus (house mouse)	
Mus musculus		Mus musculus	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
1 (bases 1 to 607)		1 (bases 1 to 607)	
Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H., Takeda,J., Ohara,O. and Seino,S.		Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H., Takeda,J., Ohara,O. and Seino,S.	
Construction of a multi-functional cDNA library specific for mouse pancreatic islets and its application to microarray		Construction of a multi-functional cDNA library specific for mouse pancreatic islets and its application to microarray	
Unpublished (2004)		Unpublished (2004)	
Contact: Susumu Seino		Contact: Susumu Seino	
Division of Cellular and Molecular Medicine		Division of Cellular and Molecular Medicine	
Kobe University Graduate School of Medicine		Kobe University Graduate School of Medicine	
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan		7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan	
Tel: 81-78-382-5360		Tel: 81-78-382-5360	
Fax: 81-78-382-5370		Fax: 81-78-382-5370	
Email: seinomed.kobe-u.ac.jp.		Email: seinomed.kobe-u.ac.jp.	
Location/Qualifiers		Location/Qualifiers	
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ORIGIN		ORIGIN	
Query Match		Query Match	
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Matches 97; Conservative 0; Mismatches 77; Indels 1; Gaps 1		Matches 97; Conservative 0; Mismatches 77; Indels 1; Gaps 1	
QY	CTTCAATGTCGAGCTCTTCGAAATGATGTCGATATACGTCATGTCATGTCACCC	QY	CTTCAATGTCGAGCTCTTCGAAATGATGTCGATATACGTCATGTCATGTCACCC
DB	CTTCATGTCGATATGAAATATTTATTAATGTTGGAAATACATTTTCATGTTTATGATACAGC	DB	CTTCATGTCGATATGAAATATTTATTAATGTTGGAAATACATTTTCATGTTTATGATACAGC
QY	GCATTATCTAAAGCTAAAGCACTGGAAAGAAATGCTGGGGCCCGAAGAATGGCAATC	QY	GCATTATCTAAAGCTAAAGCACTGGAAAGAAATGCTGGGGCCCGAAGAATGGCAATC
DB	TCAGTCTCTTAATAGAAAGCAACTGTAA-CCATATCTGCAGACCAATGCAAGAGGCACAAAT	DB	TCAGTCTCTTAATAGAAAGCAACTGTAA-CCATATCTGCAGACCAATGCAAGAGGCACAAAT
QY	AAATTGCAAGTACGCTAGCCAGTTCGAATTTAAAGCGGAATCCGAGCAATCGTG	QY	AAATTGCAAGTACGCTAGCCAGTTCGAATTTAAAGCGGAATCCGAGCAATCGTG
DB	AAACTGGAAGTGAAGAAAAAAGAAAAAAGCGCGCCGCGCAGCTTCTCTTG	DB	AAACTGGAAGTGAAGAAAAAAGAAAAAAGCGCGCCGCGCAGCTTCTCTTG
RESULT 10		RESULT 10	
LOCUS	BX62586	LOCUS	BX62586
DEFINITION	BX62586 AGENAE Gallus gallus multi-tissues normalized and	DEFINITION	BX62586 AGENAE Gallus gallus multi-tissues normalized and

Accession	Version	Keywords	Source	Organism	Reference Authors	Title	Journal	Comment
once-subtracted cDNA library (gcal)				Gallus gallus cDNA clone				
gcal0008c.h.19 5prim, mRNA sequence.								
BM62586								
EX262586.1	GI:28585184							
EST.								
Gallus gallus (chicken)								
Gallus gallus								
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.								
1 (bases 1 to 739)								
Herauld,F., Le Meunh-Metzinger,V., Desert,C., Retout,E., Piumi,F., Klopp,C. and Douaire,M.								
Construction and primary characterization of chicken normalized multi-tissue cDNA libraries								
Unpublished (2003)								
Contact: Douaire M								
INRA, UMR INRA-ENSAR Genetique Animale								
65, rue de Saint-Brieuc, RENNES cedex, 35042, FRANCE								
Tel: +33 (0) 2.23.48.54.63								
Fax: +33 (0) 2.23.48.54.70								
Email: Madeleine.Douaire@azhon.inra.fr								
Sequence cleaned of vector, adaptor and repetitions. Contact us at siemensupport@jouy.inra.fr to obtain the chromatogram of this sequence.								
Seq primer: 0008	row: h	column: 19						
Plate: M13R.								
Location/Qualifiers								
1. 739								
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/mol_type="mRNA"								
/db_xref="taxon:9031"								
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/tissue_type="multi-tissues"								
/dev_stage="from embryos to adults"								
/lab_host="DH108"								
/clone_lib="AGENAS Gallus gallus multi-tissues normalized and once-subtracted cDNA library (gcal)"								
/note="Vector: pT73D-Pac; tissues: adipose tissue, brain, kidney, liver, multi-tissues, muscle, ovary, testis, bone marrow, caecum, duodenum, embryos, fabricius gland, granulosa, hypochlamus, ileon, jejunum, oviduct, pancreas, skin, spleen, thymus, utero-vaginal gland, pituitary gland, hematopoietic progenitor cells, small follicle. Clone distribution: AGENAS Resource centre, Francois Piumi, Francois Piumi.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"								
Query Match	3.7%	Score 39.8;	DB 5;	Length 739;				
Best Local Similarity	49.8%	Pred. No. 2.7;						
Matches 101;	Conservative 0;	Mismatches 102;	Indels 0;	Gaps 0;				
382 CAGTCTCTAATGATTCATATGCGAAGCAATTAATGACGTTGCGTCAATTCCTTA	441							
231 CAGGTGTGTCCTATTTCTGATTTAAGCAAACTGTTGAAGAACTGAGAGCTGCATCA	290							
442 GCGGTTTAAGGAGAAACAACAAAAGATTTGTATTAACAAATCATATACATCCGCTC	501							
291 AGTCTTAATAATGAGAAAAACAAAAGCACTGATCTCTTATAGAACATTATCAACTTC	350							
502 AACCTAAGAAATATATTCGAAAGGCTCCGGAACCGGTGGTTCCTCATTTCAAGTCTCT	561							
351 GACCTGTGTCCTTAATTCACAGACTCCCTGGCAGCGATGATTTCTCCACCTCCCTTTACT	410							
562 TCTTTTCACTAAGCTTCTGACGA	584							
411 GCTTCACAATATGCTGCAGTGA	433							

LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

CNS0A7F8
 Arabidopsis thaliana Full-length cDNA Complete sequence from clone
 GSLTSL16F06 of Adult vegetative tissue of strain col-0 of
 Arabidopsis thaliana (thale cress).
 BX823253
 BX823253.1 GI:42466155
 HTC; GSLT cDNA.
 Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 2433)
 Castelli, V., Aury, J.M., Jallion, O., Wincker, P., Clepet, C.,
 Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
 Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.
 Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:
 A Combined Approach to Evaluate and Improve Arabidopsis Genome
 Annotation
 Unpublished
 2 (bases 1 to 2433)
 Genoscope.
 Direct Submission
 Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 The sequences are based on single pass reads.
 Life Technologies (a division of Invitrogen) members carried out
 full-length libraries construction : Temple G.
 Genoscope members carried out sequencing and annotation : Castelli
 V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C.,
 Schachter V., Weissenbach J., Salanoubat M.
 UNGV INRA : Clepet C., Caboche M.
 Annotation is based on the June 2003 version of the Arabidopsis
 genome released by MIPS (Munich Information Center for Protein
 Sequences) . 5 prime and 3 prime are assembled with Phrap.
 http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
 length
 http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
 Location/Qualifiers
 1..2433
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ORIGIN

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250 TCAGCATTTCCTCCGATATTCAGAGAGCTAAATCGAGCTCCGACGCAATCTATC 309
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 1613 TCAGAGATTCGACGCAATCTCGCGAGGCAAGCAGACCTCGACGCAAGTTTACA 1672
 310 ATCGACAGAGCGAGATACATCGAATGGGAGATTTCCAAATCGACGCGAGATCTGCC 369
 1673 AAGGGTAAGATAGAGAAAGGTTGGAATGGGAAATACATATATGATGGGAAGTTAAC 1732
 370 AGAGAGGCGCAGAGCTGCTATGATTCATATGCGGAAGCATTAATGCAAGTTGCGTT 429
 1733 AGAAGAGGAGGAGCAATGCGAGATTCGATCTATTCAGAAATATTCGCGCAATAGTCT 1792
 430 CAATTCGCTTAAGGCTTAAAGGAGGAGCAACCAAAAGT 471
 1793 AGTAACAAAAGTAGTTCCAGAGTCAGAACAGTAGTAGT 1834

RESULT 12
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BX200121
 Danio rerio genomic clone DKEX-210B11, genomic survey sequence.
 BX200121
 BX200121.1 GI:28032007
 GSS.
 Danio rerio (zebrafish)
 Danio rerio
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 738)
 Humphray, S.J., Huckle, E. and Durham, J.L.
 Direct Submission
 Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
 Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humphrey@sanger.ac.uk Unpublished
 This sequence was generated from the SP6 end of BAC 210B11. 210B11
 is part of the Daniokey BAC library created by R. Plasterk and N.V.
 Keygene. Further details:
 http://www.sanger.ac.uk/Projects/D_rerio/
 Location/Qualifiers
 1..738
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ORIGIN

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13 AAGAAATTAAGATTCAGTCAAGAACTATTTCTTAATTCCTCCAGCTCTATCT 72
 568 AAGTATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 627
 73 AAGAGAGACACTTTCCCAATTAACAACCTTAATTCCTCCAGCTCAACGAATTCATC 132
 628 AAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 687
 133 AAAATTTGAGAGAGCTTCATGAAA 157
 688 AACGTAAGTTAAAGCTTATAGAAA 712

RESULT 13
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

CC375636
 PUMH234TB ZM_0.6_1.0_KB Zea mays genomic clone ZMHBTA488E20,
 genomic survey sequence.
 CC375636
 CC375636.1 GI:30849253
 GSS.
 Zea mays
 Zea mays
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 762)
 Whiteley, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
 Bennettzen, J.
 Maize Genomics Consortium
 Unpublished (2003)
 Other GSS: PUMH234TD
 Contact: Cathy Whiteley
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843

Tue Dec 7 11:29:39 2004

us-09-491-063a-1.rst

Page 8

Search completed: December 4, 2004, 16:15:44
Job time : 3911 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2004, 14:54:43 ; Search time 157 Seconds
(Without alignments)
824.849 Million cell updates/sec

Title: US-09-491-063a-2

Sequence: 1 MPEPKKRVQSKNYFLTPQ.....PLVQESTQASQETGNKQAG 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneseqp1960s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1908	98.4	361	2	AAW34336 Tomato mo
2	1902	98.1	361	2	AAW34325 Tomato mo
3	1892	97.6	361	2	AAW34326 Tomato mo
4	1879	96.9	361	2	AAW34324 Tomato mo
5	1575	81.2	353	1	AAW34332 Bean gold
6	1572	81.1	353	2	AAW34332 Bean gold
7	1572	81.1	353	2	AAW34332 Bean gold
8	1567	80.8	353	2	AAW34333 Bean gold
9	1566	80.7	353	2	AAW34333 Bean gold
10	1564	80.7	353	2	AAW34335 Bean gold
11	1499	77.3	356	3	AAW34337 Bean gold
12	1308.5	67.5	359	2	AAW34330 Tomato ye
13	1305.5	67.3	359	2	AAW34330 Tomato ye
14	1305.5	67.3	359	2	AAW34330 Tomato ye
15	1293.5	66.7	357	2	AAW34329 Tomato ye
16	1293.5	66.7	357	2	AAW34329 Tomato ye
17	1290.5	66.6	357	2	AAW34330 Tomato ye
18	1286.5	66.6	357	2	AAW34330 Tomato ye
19	1262	65.1	362	2	AAW34331 Tomato ye
20	1242	64.1	361	1	AAW34331 Tomato ye
21	1242	64.1	361	1	AAW34331 Tomato ye
22	599	30.9	142	6	AAW34327 Tomato mo
23	486	25.1	135	3	AAW34318 Maatrevir
24	277	14.3	292	3	AAW34317 Maatrevir
25	260	13.4	264	3	AAW34317 Maatrevir

26	260	13.4	264	3	AAW34336 standard; protein; 361 AA.	AAW34336
27	257	13.3	264	8	AAW34336; (first entry)	AAW34336
28	241	12.4	143	3	AAW34336; (first entry)	AAW34336
29	224	11.6	70	3	AAW34336; (first entry)	AAW34336
30	224	11.6	70	3	AAW34336; (first entry)	AAW34336
31	218	11.2	70	3	AAW34336; (first entry)	AAW34336
32	217	11.2	70	3	AAW34336; (first entry)	AAW34336
33	216	11.1	70	3	AAW34336; (first entry)	AAW34336
34	216	11.1	70	3	AAW34336; (first entry)	AAW34336
35	214	11.0	70	3	AAW34336; (first entry)	AAW34336
36	214	11.0	70	3	AAW34336; (first entry)	AAW34336
37	212	10.9	70	3	AAW34336; (first entry)	AAW34336
38	210	10.8	70	3	AAW34336; (first entry)	AAW34336
39	210	10.8	70	3	AAW34336; (first entry)	AAW34336
40	209	10.8	70	3	AAW34336; (first entry)	AAW34336
41	208	10.7	70	3	AAW34336; (first entry)	AAW34336
42	207	10.7	70	3	AAW34336; (first entry)	AAW34336
43	200	10.3	70	3	AAW34336; (first entry)	AAW34336
44	141	7.3	27	2	AAW34336; (first entry)	AAW34336
45	137	7.1	27	2	AAW34336; (first entry)	AAW34336

ALIGNMENTS

RESULT 1	AAW34336	AAW34336 standard; protein; 361 AA.
AC	AAW34336;	
DT	17-OCT-2003 (revised)	
DT	27-APR-1998 (first entry)	
XX		
DE	Tomato mottle virus AC1 protein.	
XX		
KW	Geminivirus; TOMOV; AC1 gene; transdominant mutation; transgenic plant;	
KW	disease resistance.	
XX		
OS	Tomato mottle virus; isolate Florida.	
XX		
PN	MO9739110-A1.	
XX		
PD	23-OCT-1997.	
XX		
PF	15-APR-1997; 97MO-US006300.	
XX		
PR	16-APR-1996; 96US-0015517P.	
XX		
PA	(SEMT-) SEMINIS VEGETABLE SEEDS INC.	
PA	(WISC) WISCONSIN ALUMNI RES FOUND.	
XX		
PI	Scout UT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;	
XX		
DR	WPI; 1997-526447/48.	
XX		
PT	N-PDB; AAT93294.	
PT	Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant	
PT	genes - have increased resistance to geminivirus infection e.g. tomato	
PT	mottle virus, tomato yellow leaf curl virus or bean golden mosaic	
PT	geminivirus.	
XX		
PS	Example 3.3; Page 57-58; 132pp; English.	
XX		
CC	This protein comprises the wild-type AC1 protein of tomato mottle virus	
CC	(TOMOV), a geminivirus that has a bipartite genome. The AC1 gene (see	
CC	AAW34336) must be expressed for efficient replication of the two genomic	
CC	components, DNA-A and DNA-B. The AC1 protein has a DNA binding site	
CC	specific to the DNA-A common region, a DNA nicking activity, and an ATP	
CC	binding activity. The invention involves production of transgenic plants	
CC	containing DNA comprising AC1 or CI wild-type or mutant sequences that	
CC	negatively interfere in trans with geminiviral replication during	
CC	infection. Such transgenic plants are resistant to viral infection. The	

CC AC1/C1 genes are especially from TOMOV, tomato yellow leaf curl virus or
 CC bean golden mosaic geminivirus (see AAT93282-93) and encode polypeptides
 CC (see AAM34324-35) that have mutations in the highly conserved DNA-nicking
 CC domain and/or the NTP-binding domain. (Updated on 17-Oct-2003 to
 CC standardise OS field)

XX Sequence 361 AA;

Query Match 98.4%; Score 1908; DB 2; Length 361;
 Best Local Similarity 98.3%; Pred. No. 4.5e-169;
 Matches 355; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPPKRRVQSKNYFLTYPCSLSKERALSQLNLNTPVKKFKIKICREIHENGEPHLHV 60
 DB 1 MPPKRRVQSKNYFLTYPCSLSKERALSQLNLNTPVKKFKIKICREIHENGEPHLHV 60
 QY 61 LVQEGKYQCTNNRFPDLVSPTRSAHPHPNIQAKSSDVKSYIDKGDITLWGDFOIDG 120
 DB 61 LVQEGKYQCTNNRFPDLVSPTRSAHPHPNIQAKSSDVKSYIDKGDITLWGDFOIDG 120
 QY 121 RSARGGQGSANDSYAKALNAGVSQALAVLREBPQKDFVLQNNHNRSLERIFAKAPEPW 180
 DB 121 RSARGGQGSANDSYAKALNAGVSQALAVLREBPQKDFVLQNNHNRSLERIFAKAPEPW 180
 QY 181 VPPFQVSSFTNVPEDEMADNYPGTGDAAPDRPVSIIVEGDSRTGKTWABALGPHNY 240
 DB 181 VPPFQVSSFTNVPEDEMADNYPGTGDAAPDRPVSIIVEGDSRTGKTWABALGPHNY 240
 QY 241 LSGHLDNNGRVFNSNDVQYVNIIDIAHPHYLKLKMKKELGAKQKQMSCKYKGPVQIKGI 300
 DB 241 LSGHLDNNGRVFNSNDVQYVNIIDIAHPHYLKLKMKKELGAKQKQMSCKYKGPVQIKGI 300
 QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNMTIKNAIFITLTAPLYOESTQASQETGNQKQ 360
 DB 301 PAIVLCNPGEGASYKEFLDKAENTGLKNMTIKNAIFITLTAPLYOESTQASQETGNQKQ 360
 QY 361 G 361
 DB 361 G 361

RESULT 2
 AAM34325
 ID AAM34325 standard; protein; 361 AA.

XX AAM34325;

XX 27-APR-1998 (first entry)

DE Tomato mottle virus AC1 mutant TOMV-AC1d1m1.

KM Geminivirus; TOMOV-AC1d1m1; AC1 gene; transdominant mutation;

KM transgenic plant; disease resistance.

OS Tomato mottle virus; isolate Florida.

OS Synthetic.

XX MO9739110-A1.

XX 23-OCT-1997.

XX 15-APR-1997; 97WO-US006300.

XX 16-APR-1996; 96US-0015517P.

XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.

XX (WISC) WISCONSIN ALUMNI RES FOUND.

XX Stout UT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;

XX WPI, 1997-526447/48.

XX N-PSDB; AAT93283.

PT Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant
 PT genes - have increased resistance to geminivirus infection e.g. tomato
 PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic
 PT geminivirus.

XX Example 3.5; Page 64-65; 132pp; English.

CC This protein comprises a transdominant lethal mutant, designated TOMOV-
 CC AC1d1m1, of tomato mottle virus (TOMOV) AC1 protein (see AAM34336). It is
 CC encoded by a mutant AC1 gene (see AAT93283) of tomato mottle virus
 CC (TOMOV), and carries a mutation in an NTP-binding domain. The AC1 gene
 CC (see also AAM34394) must be expressed for efficient replication of the
 CC two genomic components, DNA-A and DNA-B, of the bipartite TOMOV genome.
 CC The invention involves production of transgenic plants containing DNA
 CC comprising geminivirus AC1 or C1 wild-type or mutant sequences that
 CC negatively interfere in trans with geminiviral replication during
 CC infection. Such transgenic plants are resistant to viral infection. The
 CC AC1/C1 genes are especially from TOMOV, tomato yellow leaf curl virus or
 CC bean golden mosaic geminivirus (see AAT93282-93) and encode polypeptides
 CC (see AAM34324-35) that have mutations in the highly conserved DNA-nicking
 CC and/or NTP-binding domains

XX Sequence 361 AA;

Query Match 98.1%; Score 1902; DB 2; Length 361;
 Best Local Similarity 98.1%; Pred. No. 1.6e-168;
 Matches 354; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPPKRRVQSKNYFLTYPCSLSKERALSQLNLNTPVKKFKIKICREIHENGEPHLHV 60
 DB 1 MPPKRRVQSKNYFLTYPCSLSKERALSQLNLNTPVKKFKIKICREIHENGEPHLHV 60
 QY 61 LVQEGKYQCTNNRFPDLVSPTRSAHPHPNIQAKSSDVKSYIDKGDITLWGDFOIDG 120
 DB 61 LVQEGKYQCTNNRFPDLVSPTRSAHPHPNIQAKSSDVKSYIDKGDITLWGDFOIDG 120
 QY 121 RSARGGQGSANDSYAKALNAGVSQALAVLREBPQKDFVLQNNHNRSLERIFAKAPEPW 180
 DB 121 RSARGGQGSANDSYAKALNAGVSQALAVLREBPQKDFVLQNNHNRSLERIFAKAPEPW 180
 QY 181 VPPFQVSSFTNVPEDEMADNYPGTGDAAPDRPVSIIVEGDSRTGKTWABALGPHNY 240
 DB 181 VPPFQVSSFTNVPEDEMADNYPGTGDAAPDRPVSIIVEGDSRTGKTWABALGPHNY 240
 QY 241 LSGHLDNNGRVFNSNDVQYVNIIDIAHPHYLKLKMKKELGAKQKQMSCKYKGPVQIKGI 300
 DB 241 LSGHLDNNGRVFNSNDVQYVNIIDIAHPHYLKLKMKKELGAKQKQMSCKYKGPVQIKGI 300
 QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNMTIKNAIFITLTAPLYOESTQASQETGNQKQ 360
 DB 301 PAIVLCNPGEGASYKEFLDKAENTGLKNMTIKNAIFITLTAPLYOESTQASQETGNQKQ 360
 QY 361 G 361
 DB 361 G 361

RESULT 3
 AAM34326
 ID AAM34326 standard; protein; 361 AA.

XX AAM34326;

XX 27-APR-1998 (first entry)

DE Tomato mottle virus AC1 mutant TOMV-AC1d1m23.

KM Geminivirus; TOMOV-AC1d1m23; AC1 gene; transdominant mutation;

KM transgenic plant; disease resistance.

XX Tomato mottle virus; isolate Florida.

XX Synthetic.

PN MO9739110-A1.
 XX AAW34324
 PD 23-OCT-1997.
 XX
 PF 15-APR-1997; 97MO-US006300.
 XX
 PR 16-APR-1996; 96US-0015517P.
 XX
 PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 XX
 PI Scout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;
 DR WPI, 1997-526447/48.
 DR N-PSDB; AAT93284.
 XX
 PT Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
 PT genes - have increased resistance to geminivirus infection e.g. tomato
 PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic
 PT geminivirus.
 XX
 PS Example 3.6; Page 67-69; 132pp; English.
 XX
 CC This protein comprises a transdominant lethal mutant, designated ToMoV-
 CC AC1d1m23, of tomato mottle virus (ToMoV) AC1 protein (see AAW34336). It
 CC is encoded by a mutant AC1 gene (see AAT93284) of tomato mottle virus
 CC virus (ToMoV), and carries 2 mutations in an NTP-binding domain. The AC1
 CC gene (see also AAT93294) must be expressed for efficient replication of
 CC the two genomic components, DNA-A and DNA-B, of the bipartite ToMoV
 CC genome. The invention involves production of transgenic plants containing
 CC DNA comprising geminivirus AC1 or CI wild-type or mutant sequences that
 CC negatively interfere in trans with geminiviral replication during
 CC infection. Such transgenic plants are resistant to viral infection. The
 CC AC1/CI genes are especially from ToMoV, tomato yellow leaf curl virus or
 CC bean golden mosaic geminivirus (see AAT93282-93) and encode polypeptides
 CC (see AAW34324-35) that have mutations in the highly conserved DNA-nicking
 CC and/or NTP-binding domains
 XX
 XX Sequence 361 AA;
 SQ
 Query Match 97.6%; Score 1892; DB 2; Length 361;
 Best Local Similarity 97.8%; Pred. No. 1.4e-167;
 Matches 351; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MPPPKKFRVQSKNYFLTYPCSLSKKEBALSQLONTLPVKKFKIKICREIHENGEPHLAV 60
 DB 1 MPPPKKFRVQSKNYFLTYPCSLSKKEBALSQLONTLPVKKFKIKICREIHENGEPHLAV 60
 QY 61 LVQPEGRYQCTNNRFPDLVSPTRSAHFHPIIOGAKSSDVKSYIDKDGDTIEWGDFQIDG 120
 DB 61 LVQPEGRYQCTNNRFPDLVSPTRSAHFHPIIOGAKSSDVKSYIDKDGDTIEWGDFQIDG 120
 QY 121 RSARGGQOSANDSYAKALNAGSVOSALAVIREOPKDFVLQNNHINSNLERIPAKAPEPW 180
 DB 121 RSARGGQOSANDSYAKALNAGSVOSALAVIREOPKDFVLQNNHINSNLERIPAKAPEPW 180
 QY 121 RSARGGQOSANDSYAKALNAGSVOSALAVIREOPKDFVLQNNHINSNLERIPAKAPEPW 180
 DB 121 RSARGGQOSANDSYAKALNAGSVOSALAVIREOPKDFVLQNNHINSNLERIPAKAPEPW 180
 QY 181 VPPFOVSSFTNNVDEQEMADNYFGTGDAAPPRPVSIIIEGDSRTGKTMMARALGPHNY 240
 DB 181 VPPFOVSSFTNNVDEQEMADNYFGTGDAAPPRPVSIIIEGDSRTGKTMMARALGPHNY 240
 QY 241 LSGHLDPNNGVFPNDVQYNYIDIAPIHYLKLKMKKELGAKQWQOSCKYKGPQIRGGI 300
 DB 241 LSGHLDPNNGVFPNDVQYNYIDIAPIHYLKLKMKKELGAKQWQOSCKYKGPQIRGGI 300
 QY 301 PAVLVCNPGEGASKEFLDKAENTGLKNWTIKNAIFITLLTAPLYQESTQASOETGNQKQ 360
 DB 301 PAVLVCNPGEGASKEFLDKAENTGLKNWTIKNAIFITLLTAPLYQESTQASOETGNQKQ 360
 QY 361 G 361
 DB 361 G 361

RESULT 4
 AAW34324
 ID AAW34324 standard; protein; 361 AA.
 XX
 AC AAW34324;
 XX
 DT 27-APR-1998 (first entry)
 XX
 XX Tomato mottle virus AC1 mutant ToMoV-AC1d1m.
 DE Geminivirus; ToMoV-AC1d1m; AC1 gene; transdominant mutation;
 KM transgenic plant; disease resistance.
 XX
 OS Tomato mottle virus; isolate Florida.
 OS Synthetic.
 XX
 PN MO9739110-A1.
 XX
 PD 23-OCT-1997.
 XX
 PF 15-APR-1997; 97MO-US006300.
 XX
 PR 16-APR-1996; 96US-0015517P.
 XX
 PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 XX
 PI Scout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;
 DR WPI, 1997-526447/48.
 DR N-PSDB; AAT93282.
 XX
 PT Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
 PT genes - have increased resistance to geminivirus infection e.g. tomato
 PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic
 PT geminivirus.
 XX
 PS Example 3.4; Page 60-62; 132pp; English.
 XX
 CC This protein comprises a transdominant lethal mutant, designated ToMoV-
 CC AC1d1m, of tomato mottle virus (ToMoV) AC1 protein (see AAW34336). It is
 CC encoded by a mutant AC1 gene (see AAT93282) of tomato mottle virus
 CC virus (ToMoV), and carries 3 mutations in its NTP-binding domains. The AC1 gene
 CC (see also AAT93294) must be expressed for efficient replication of the
 CC two genomic components, DNA-A and DNA-B, of the bipartite ToMoV genome.
 CC The invention involves production of transgenic plants containing DNA
 CC comprising geminivirus AC1 or CI wild-type or mutant sequences that
 CC negatively interfere in trans with geminiviral replication during
 CC infection. Such transgenic plants are resistant to viral infection. The
 CC AC1/CI genes are especially from ToMoV, tomato yellow leaf curl virus or
 CC bean golden mosaic geminivirus (see AAT93282-93) and encode polypeptides
 CC (see AAW34324-35) that have mutations in the highly conserved DNA-nicking
 CC and/or NTP-binding domains
 XX
 XX Sequence 361 AA;
 SQ
 Query Match 96.9%; Score 1879; DB 2; Length 361;
 Best Local Similarity 97.2%; Pred. No. 2.3e-166;
 Matches 351; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 1 MPPPKKFRVQSKNYFLTYPCSLSKKEBALSQLONTLPVKKFKIKICREIHENGEPHLAV 60
 DB 1 MPPPKKFRVQSKNYFLTYPCSLSKKEBALSQLONTLPVKKFKIKICREIHENGEPHLAV 60
 QY 61 LVQPEGRYQCTNNRFPDLVSPTRSAHFHPIIOGAKSSDVKSYIDKDGDTIEWGDFQIDG 120
 DB 61 LVQPEGRYQCTNNRFPDLVSPTRSAHFHPIIOGAKSSDVKSYIDKDGDTIEWGDFQIDG 120
 QY 121 RSARGGQOSANDSYAKALNAGSVOSALAVIREOPKDFVLQNNHINSNLERIPAKAPEPW 180
 DB 121 RSARGGQOSANDSYAKALNAGSVOSALAVIREOPKDFVLQNNHINSNLERIPAKAPEPW 180
 QY 181 VPPFOVSSFTNNVDEQEMADNYFGTGDAAPPRPVSIIIEGDSRTGKTMMARALGPHNY 240
 DB 181 VPPFOVSSFTNNVDEQEMADNYFGTGDAAPPRPVSIIIEGDSRTGKTMMARALGPHNY 240

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Db      181 VPPQVSSFTNVPEBEMADNFTGTGAARPERPVSIIVEGDSRTGHTMMARALGPHNY 240
Qy      241 LSGHLDNGRVFSNDVQYNNVIDIAPHYLKLKHWKELGAKQKMQSNCKTGKPVQIKGI 300
Db      241 LSGHLDNGRVFSNDVQYNNVIDIAPHYLKLKHWKELGAKQKMQSNCKTGKPVQIKGI 300
Qy      301 PAIVLCNPGGASGYKEFLDKAENTGLKNMTIKNAIFITLAPLYQESTQASQEPGNQKQ 360
Db      301 PAIVLCNPGGASGYKEFLDKAENTGLKNMTIKNAIFITLAPLYQESTQASQEPGNQKQ 360
Qy      361 G 361
Db      361 G 361

RESULT 5
AAP70407
ID AAP70407 standard; protein, 353 AA.
XX
AC AAP70407;
XX
XX 25-MAR-2003 (revised)
DT 02-MAY-1991 (first entry)
XX
DE ORF 4 gene product of Bean Golden Mosaic virus.
XX
XX Plant vector.
XX
XX Bean golden mosaic virus.
XX
XX JP61257186-A.
XX
XX 14-NOV-1986.
XX
XX 10-MAY-1985; 85JP-00098108.
XX
XX 10-MAY-1985; 85JP-00098108.
XX
XX (TEIJU) TEIJUN LTD.
XX
XX WPI; 1987-159662/23.
DR N-PSDB; AAN70630.
XX
XX New DNA and hybrid DNA - used for recombinant vector of plants.
XX
XX PS Disclosure; Fig 6; 24pp; Japanese.
XX
XX The sequence encoding this protein may be taken along with the -a DNA
CC sequence and a suitable resistance gene, and used to create a recombinant
CC plant vector. See also AAN70629. (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
XX Sequence 353 AA;
XX
Query Match 81.2%; Score 1575; DB 1; Length 353;
Best Local Similarity 79.8%; Pred. No. 5.4e-138; Indels 0; Gaps 0;
Matches 281; Conservative 34; Mismatches 37;
Qy      1 MPPPKFRVOSKYNFLTYPOCSLSKEBALSQLQNLNTPVNKKFKIKRELHENGEPHLAV 60
Db      1 MPPPKFRVOSKYNFLTYPRCTIPKEALSQLOKHITTTNKKFKIKVEBRHDNGBPHLA 60
Qy      61 LVQFEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVKSYIDKGGDTIEMGDFQIDG 120
Db      61 LIQEGFKICTNKLFDLVSTTRSAHFHPNIQAKSSDVKSYIDKGGDTIEMGDFQIDG 120
Qy      121 RSARGGQOSANDSYAKALNAGVQSALAVREEQPKDFVLQNHNRISNLERIFAKAPEPW 180
Db      121 RSARGGQOSANDSYAKALNADISALTILKEQPKDFVLQNHNRISNLERIFKVEBEPW 180
Qy      181 VPPQVSSFTNVPEBEMADNFTGTGAAPDRPVSIIVEGDSRTGHTMMARALGPHNY 240

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Db      181 VPPPLSSFVNIPVWQMDWYDFGRGSAARPERPVSIIVEGDSRTGHTMMARALGPHNY 240
Qy      241 LSGHLDNGRVFSNDVQYNNVIDIAPHYLKLKHWKELGAKQKMQSNCKTGKPVQIKGI 300
Db      241 LSGHLDNSRVSVSNVYNNVIDISPNYLKLKHWKELGAKQKMQSNCKTGKPVQIKGI 300
Qy      301 PAIVLCNPGGASGYKEFLDKAENTGLKNMTIKNAIFITLAPLYQESTQASQ 352
Db      301 PSIVLCNPGGSSYKDFLNKEENRALHNTIHNALFVTLAPLYQSTADQDQ 352

RESULT 6
AAM34332
ID AAM34332 standard; protein, 353 AA.
XX
XX AAM34332;
XX
XX 17-OCT-2003 (revised)
DT 27-APR-1998 (first entry)
XX
DE Bean golden mosaic geminivirus CI BGA190 mutant.
XX
XX Geminivirus; BGMY; CI gene; transdominant mutation; transgenic plant;
XX disease resistance.
XX
XX Bean golden mosaic virus; type II isolate Guatemala.
XX
XX W09739110-A1.
XX
XX 23-OCT-1997.
XX
XX 15-APR-1997; 97WO-US006300.
XX
XX 16-APR-1996; 96US-0015517P.
XX
XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.
PA (WISC-) WISCONSIN ALUMNI RES FOUND.
XX
XX Scout UT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;
XX
XX WPI; 1997-526447/48.
DR N-PSDB; AAT93290.
XX
XX Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
PT genes - have increased resistance to geminivirus infection e.g. tomato
PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic
PT geminivirus.
XX
XX PS Example 5; Page 103-105; 132pp; English.
XX
XX This protein comprises a control mutant of the bean golden mosaic virus
CC (BGMY) CI protein (see AAM34338) that is required for replication. It is
CC encoded by mutated CI open reading frame BGAC190 (see AAT93290). The
CC invention involves production of transgenic plants containing DNA
CC comprising geminivirus CI or AC1 wild-type or mutant sequences that
CC negatively interfere in trans with geminiviral replication during
CC infection. Such transgenic plants are resistant to viral infection. The
CC AC1/CI genes are especially from BGMY, tomato mottle virus or tomato
CC yellow leaf curl virus (see AAT93282-93) and encode polypeptides (see
CC AAM34324-35) that have mutations in the highly conserved DNA-nicking
CC and/or the ATP-binding domains. (Updated on 17-OCT-2003 to standardise OS
CC field)
XX
XX Sequence 353 AA;
XX
Query Match 81.1%; Score 1572; DB 2; Length 353;
Best Local Similarity 80.4%; Pred. No. 1e-137; Indels 0; Gaps 0;
Matches 283; Conservative 31; Mismatches 38;
Qy      1 MPPPKFRVOSKYNFLTYPOCSLSKEBALSQLQNLNTPVNKKFKIKRELHENGEPHLAV 60
Db      1 MPPPKFRVOSKYNFLTYPRCTIPKEALVLSQLOKHITATNKKFKIKVEBRHENGEPHLA 60

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CC geminivirus CI or AC1 wild-type or mutant sequences that negatively
 CC interfere in trans with geminiviral replication during infection. Such
 CC transgenic plants are resistant to viral infection. The AC1/CI genes are
 CC especially from BGWV, tomato mottle virus or tomato yellow leaf curl
 CC virus (see AAT93282-93) and encode polypeptides (see AAM34324-35) that
 CC have mutations in the highly conserved DNA-nicking and/or the NTP-binding
 CC domains. (Updated on 17-OCT-2003 to standardise OS field)
 CC XX
 SQ Sequence 353 AA;
 Query Match 80.8%; Score 1567; DB 2; Length 353;
 Best Local Similarity 80.1%; Pred. No. 3e-137;
 Matches 282; Conservative 31; Mismatches 39; Indels 0; Gaps 0;
 QY 1 MPPPKRRVQSKNYFLTYPCQSLSKERALSQLNLNTPVKKFKIKICRELHENGEPHLAV 60
 DB 1 MPPPKRRVQSKNYFLTYPCQSLSKERALSQLNLNTPVKKFKIKICRELHENGEPHLA 60
 QY 61 LVQPEGKYQCTNNRFPDLVSPTRSAHPHPIQAKSSSDVKSYYIDKDGDTIEMGDFQIDG 120
 DB 61 LIQPEGKVCCTNKRFLDLVSTSTRSAPHPHPIQAKSSSDVKSYYIDKDGVTIEMGDFQVDG 120
 QY 121 RSARGGQOSANDSYAKALNAGVOSALAVTREBOPKDFVTONNIRSNLERIFAKADEPW 180
 DB 121 RSARGGQOSANDSYAKALNAGVOSALAVTREBOPKDFVTONNIRSNLERIFAKADEPW 180
 QY 181 VPPFOVSSFTNVPDEMOMADNYFGTGDAPDPDPVSIIVEGDSRTGKTMMARALGPHNY 240
 DB 181 VPPFOVSSFTNVPDEMOMADNYFGTGDAPDPDPVSIIVEGDSRTGKTMMARALGPHNY 240
 QY 241 LSGHLDPNRGRVFNVDQYNYIDIAPIYKLKIKWKEILGAQKQWQSNCKYKGVQIKGCI 300
 DB 241 LSGHLDPNRGRVFNVDQYNYIDIAPIYKLKIKWKEILGAQKQWQSNCKYKGVQIKGCI 300
 QY 301 PAIVLCNPGGAGSYKEFLDKAENTGLKNWTIKKAIFITTLAPLYQSTTQASQ 352
 DB 301 PSIVLCNPGGAGSYKEFLDKAENTGLKNWTIKKAIFITTLAPLYQSTTQDCQ 352
 RESULT 9
 AAM34334
 ID AAM34334 standard; protein; 353 AA.
 AC AAM34334;
 XX
 XX 17-OCT-2003 (revised)
 DT 27-APR-1998 (first entry)
 DE Bean golden mosaic geminivirus CI BGA228 mutant.
 XX
 XX Geminivirus; BGWV; CI gene; transdominant mutation; transgenic plant;
 KM disease resistance.
 OS Bean golden mosaic virus; type II isolate Guatemala.
 OS WO9739110-A1.
 XX
 XX 23-OCT-1997.
 PD
 XX 15-APR-1997; 97WO-US006300.
 PF
 XX 16-APR-1996; 96US-0015517P.
 PR
 XX (SEMT-) SEMINIS VEGETABLE SEEDS INC.
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 XX
 XX Scout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;
 XX WPI; 1997-526447/48.
 DR N-PSDB; AAT93292.
 XX
 PT Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
 PT genes - have increased resistance to geminivirus infection e.g. tomato

PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic
 PT geminivirus.
 XX
 XX Example 5; Page 111-112; 132pp; English.
 PS
 XX This protein comprises a transdominant lethal mutant of the bean golden
 CC mosaic virus (BGWV) CI protein (see AAM34338) that is required for
 CC replication. It is encoded by mutated CI open reading frame BGA228 (see
 CC AAT93292) and carries a mutation in the NTP-binding domain. The invention
 CC involves production of transgenic plants containing DNA comprising
 CC geminivirus CI or AC1 wild-type or mutant sequences that negatively
 CC interfere in trans with geminiviral replication during infection. Such
 CC transgenic plants are resistant to viral infection. The AC1/CI genes are
 CC especially from BGWV, tomato mottle virus or tomato yellow leaf curl
 CC virus (see AAT93282-93) and encode polypeptides (see AAM34324-35) that
 CC have mutations in the highly conserved DNA-nicking and/or the NTP-binding
 CC domains. (Updated on 17-OCT-2003 to standardise OS field)
 CC XX
 SQ Sequence 353 AA;
 Query Match 80.8%; Score 1566; DB 2; Length 353;
 Best Local Similarity 80.1%; Pred. No. 3.7e-137;
 Matches 282; Conservative 31; Mismatches 39; Indels 0; Gaps 0;
 QY 1 MPPPKRRVQSKNYFLTYPCQSLSKERALSQLNLNTPVKKFKIKICRELHENGEPHLAV 60
 DB 1 MPPPKRRVQSKNYFLTYPCQSLSKERALSQLNLNTPVKKFKIKICRELHENGEPHLA 60
 QY 61 LVQPEGKYQCTNNRFPDLVSPTRSAHPHPIQAKSSSDVKSYYIDKDGDTIEMGDFQIDG 120
 DB 61 LIQPEGKVCCTNKRFLDLVSTSTRSAPHPHPIQAKSSSDVKSYYIDKDGVTIEMGDFQVDG 120
 QY 121 RSARGGQOSANDSYAKALNAGVOSALAVTREBOPKDFVTONNIRSNLERIFAKADEPW 180
 DB 121 RSARGGQOSANDSYAKALNAGVOSALAVTREBOPKDFVTONNIRSNLERIFAKADEPW 180
 QY 181 VPPFOVSSFTNVPDEMOMADNYFGTGDAPDPDPVSIIVEGDSRTGKTMMARALGPHNY 240
 DB 181 VPPFOVSSFTNVPDEMOMADNYFGTGDAPDPDPVSIIVEGDSRTGKTMMARALGPHNY 240
 QY 241 LSGHLDPNRGRVFNVDQYNYIDIAPIYKLKIKWKEILGAQKQWQSNCKYKGVQIKGCI 300
 DB 241 LSGHLDPNRGRVFNVDQYNYIDIAPIYKLKIKWKEILGAQKQWQSNCKYKGVQIKGCI 300
 QY 301 PAIVLCNPGGAGSYKEFLDKAENTGLKNWTIKKAIFITTLAPLYQSTTQASQ 352
 DB 301 PSIVLCNPGGAGSYKEFLDKAENTGLKNWTIKKAIFITTLAPLYQSTTQDCQ 352
 RESULT 10
 AAM34335
 ID AAM34335 standard; protein; 353 AA.
 AC AAM34335;
 XX
 XX 17-OCT-2003 (revised)
 DT 27-APR-1998 (first entry)
 DE Bean golden mosaic geminivirus CI BGA262 mutant.
 XX
 XX Geminivirus; BGWV; CI gene; transdominant mutation; transgenic plant;
 KM disease resistance.
 OS Bean golden mosaic virus; type II isolate Guatemala.
 OS WO9739110-A1.
 XX
 XX 23-OCT-1997.
 PD
 XX 15-APR-1997; 97WO-US006300.
 PF
 XX 16-APR-1996; 96US-0015517P.
 PR
 XX

PA (SEM-) SEMINIS VEGETABLE SEEDS INC.
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 XX Scout UT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;
 XX MPI: 1997-526447/48.
 DR N-PSDB; AAT93293.
 XX Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
 PT genes - have increased resistance to geminivirus infection e.g. tomato
 PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic
 PT geminivirus.
 XX Example 5, Page 115-116, 132pp; English.
 XX This protein comprises a transdominant lethal mutant of the bean golden
 CC mosaic virus (BGMV) CI protein (see AAW34338) that is required for
 CC replication. It is encoded by mutated CI open reading frame BGAC262 (see
 CC AAT93293) and carries a mutation in the NTP-binding domain. The invention
 CC involves production of transgenic plants containing DNA comprising
 CC geminivirus CI or AC1 wild-type or mutant sequences that negatively
 CC interfere in trans with geminiviral replication during infection. Such
 CC transgenic plants are resistant to viral infection. The AC1/CI genes are
 CC especially from BGMV, tomato mottle virus or tomato yellow leaf curl
 CC virus (see AAT93282-93) and encode polypeptides (see AAW34324-35) that
 CC have mutations in the highly conserved DNA-nicking and/or the NTP-binding
 CC domains. (Updated on 17-OCT-2003 to standardise OS field)
 CC XX
 SQ Sequence 353 AA;
 Query Match 80.7%; Score 1564; DB 2; Length 353;
 Best Local Similarity 80.1%; Pred. No. 5.7e-137;
 Matches 282; Conservative 31; Mismatches 39; Indels 0; Gaps 0;
 QY 1 MPPPKFRVQSKYFLTYPCQSLSKESALSQLNLNTPVKKFKIKCRELHENGEPHLHV 60
 Db 1 MPPPKFRVQSKYFLTYPCQSLSKESALSQLNLNTPVKKFKIKCRELHENGEPHLHV 60
 QY 61 LVQFEKRYOCTNNRFPDLVSPTRSAHFHNPNIQAKSSSDVKSXYIDKDGDTIEWGDFQIDG 120
 Db 61 LVQFEKRYOCTNNRFPDLVSPTRSAHFHNPNIQAKSSSDVKSXYIDKDGDTIEWGDFQIDG 120
 QY 121 RSRAGGQOQSANDSYAALNAGSVQALAVLREBPQDFVLQNNHNSNLERIPAKAPEPW 180
 Db 121 RSRAGGQOQSANDSYAALNAGSVQALAVLREBPQDFVLQNNHNSNLERIPAKAPEPW 180
 QY 181 VPPFOVSSFTNVDEQEWADNYFGTGDAPPRPVSIIVEGDSRTGKTMARALGPBNY 240
 Db 181 VPPFOVSSFTNVDEQEWADNYFGTGDAPPRPVSIIVEGDSRTGKTMARALGPBNY 240
 QY 241 LSGHLDPNGRVPSNDVQYNNVIDDIAPHYLKLKMKWELGAQKDMQSNCKYKGEVQIKGI 300
 Db 241 LSGHLDPNGRVPSNDVQYNNVIDDIAPHYLKLKMKWELGAQKDMQSNCKYKGEVQIKGI 300
 QY 301 PAIVLCNPGSGASYKFLDKAENTGLKNTTIKKAIFITLTAPLYQSTQASQ 352
 Db 301 PAIVLCNPGSGASYKFLDKAENTGLKNTTIKKAIFITLTAPLYQSTQASQ 352
 RESULT 11
 AAB18687
 ID AAB18687 standard; peptide; 356 AA.
 XX AAB18687;
 XX 22-JAN-2001 (first entry)
 XX Amino acid sequence of a geminivirus replication protein of TMV.
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KM ribosome binding region; resistance; geminivirus infection.
 XX Tomato golden mosaic virus.

XX Key Location/Qualifiers
 FH Misc-difference 354
 FT /note= "unspecified amino acid"
 XX
 XX W0200054573-A1.
 XX
 XX 21-SEP-2000.
 XX
 PD 15-MAR-2000; 2000MO-US006759.
 PF 18-MAR-1999; 99US-0125004P.
 PR 09-APR-1999; 99US-00289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA Hanley-Bowdoin L, Orozco BM, Kong L;
 PI MPI, 2000-618851/59.
 DR
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region.
 XX
 XX Disclosure, Page 47-48; 73pp; English.
 PS
 XX The present sequence represents a geminivirus replication (Rep) protein,
 CC which is also known as AL1. AL1 binds double-stranded DNA, catalyses
 CC cleavage and ligation of single-stranded DNA, and interacts with other
 CC viral and host proteins. Mutants of the AL1 protein are used to produce
 CC transgenic plants. The mutation in AL1 is present in a ribosome binding
 CC region, and expression of mutant AL1 protein imparts increased resistance
 CC to geminivirus infection in the plant. Mutant AL1 proteins are useful for
 CC producing plants having increased resistance or reduced sensitivity to a
 CC geminivirus such as tomato golden mosaic virus, tomato mottle virus,
 CC tomato yellow leaf curl virus, tomato leaf curl virus, African cassava
 CC mosaic virus, Indian cassava mosaic virus, potato yellow mosaic virus,
 CC bean golden mosaic virus, bean dwarf mosaic virus, squash leaf curl
 CC virus, Texas pepper virus, cotton leaf curl virus or beet curly top virus
 CC XX
 SQ Sequence 356 AA;
 Query Match 77.3%; Score 1499; DB 3; Length 356;
 Best Local Similarity 74.4%; Pred. No. 6.8e-131;
 Matches 265; Conservative 45; Mismatches 46; Indels 0; Gaps 0;
 QY 1 MPPPKFRVQSKYFLTYPCQSLSKESALSQLNLNTPVKKFKIKCRELHENGEPHLHV 60
 Db 1 MPPPKFRVQSKYFLTYPCQSLSKESALSQLNLNTPVKKFKIKCRELHENGEPHLHV 60
 QY 61 LVQFEKRYOCTNNRFPDLVSPTRSAHFHNPNIQAKSSSDVKSXYIDKDGDTIEWGDFQIDG 120
 Db 61 LVQFEKRYOCTNNRFPDLVSPTRSAHFHNPNIQAKSSSDVKSXYIDKDGDTIEWGDFQIDG 120
 QY 121 RSRAGGQOQSANDSYAALNAGSVQALAVLREBPQDFVLQNNHNSNLERIPAKAPEPW 180
 Db 121 RSRAGGQOQSANDSYAALNAGSVQALAVLREBPQDFVLQNNHNSNLERIPAKAPEPW 180
 QY 181 VPPFOVSSFTNVDEQEWADNYFGTGDAPPRPVSIIVEGDSRTGKTMARALGPBNY 240
 Db 181 VPPFOVSSFTNVDEQEWADNYFGTGDAPPRPVSIIVEGDSRTGKTMARALGPBNY 240
 QY 241 LSGHLDPNGRVPSNDVQYNNVIDDIAPHYLKLKMKWELGAQKDMQSNCKYKGEVQIKGI 300
 Db 241 LSGHLDPNGRVPSNDVQYNNVIDDIAPHYLKLKMKWELGAQKDMQSNCKYKGEVQIKGI 300
 QY 301 PAIVLCNPGSGASYKFLDKAENTGLKNTTIKKAIFITLTAPLYQSTQASQSTGN 356
 Db 301 PAIVLCNPGSGASYKFLDKAENTGLKNTTIKKAIFITLTAPLYQSTQASQSTGN 356
 RESULT 12
 AAR88872

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ID AAR8872 standard; protein; 359 AA.
XX
AC AAR8872;
XX
DT 27-AUG-2003 (revised)
DT 07-NOV-1996 (first entry)
XX
DE Sardinian tomato yellow leaf curl virus mutated Rep protein (K227R).
XX
KW Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
KW modification; mutation; viral replication; deficient; inhibition;
KW viral resistance; geminivirus; tomato yellow leaf curl virus;
KW Sardinian isolate; STYLCV; transgenic plant; P-loop; C1 protein;
KW A11 protein.
XX
OS Tomato yellow leaf curl virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 227
FT /note= "wild-type Lys has been replaced by Arg"
XX
XX WO9608573-A1.
XX
XX 21-MAR-1996.
XX
XX 15-SEP-1995; 95WO-FR001192.
XX
XX 15-SEP-1994; 94FR-00011040.
XX
XX (CNRS ) CENT NAT RECH SCI.
XX
XX Gronenborn B;
XX
XX WPI; 1996-179947/18.
XX
XX N-PSDB; AAT12906.
XX
XX Prodn. of virus-resistant transgenic plants - using mutated genomic
XX sequence from phytopathogenic DNA virus.
XX
XX Disclosure; Fig 13; 93pp; French.
XX
XX Mutation of consensus amino acids in the NTP-binding site of geminivirus
XX Rep protein is used to produce replication deficient viruses. The mutated
XX viral nucleic acid is used for producing transgenic plants that are
XX resistant to, or tolerant of, the native virus. The present sequence is a
XX mutant form of the Rep (or C1) protein from the Sardinian isolate of
XX tomato yellow leaf curl virus (STYLCV) in which the wild-type Lys227
XX residue has been changed to an Arg residue; transgenic Nicotiana
XX benthamiana plants generated by transformation with the mutated virus
XX were not resistant to STYLCV. In contrast, plants transformed with a
XX virus in which Lys227 had been replaced by Ala were found to be
XX resistant. (Updated on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 359 AA;
XX
Query Match 67.5%; Score 1308.5; DB 2; Length 359;
Best Local Similarity 66.0%; Pred. No. 4.2e-113;
Matches 239; Conservative 49; Mismatches 65; Indels 9; Gaps 4;
QY 1 MPPPKKRRVOSKNVFLTYPOCSLSKEBALSQLONTNTPVKKFKIKICREIHENGEPLHAY 60
DB 1 MPPSGRPSIAKKNVFLTYPKCDLTKENALSGITVLQPTNKLFIKICREIHENGEPLHAI 60
QY 61 LVQFEGKYOCNTNRPFLVSPTRSAHFHPNIQAKSSDVKSYIDKQDGTLEWDFQIDG 120
DB 61 LIFEGKYCNCNTNCFDLVSPTRSAHFHPNIQAKSSDVKSYIDKQDVLIEWGTFOIDG 120
QY 121 RSARGGQOSANDSYAKALNNGSVQALAVLEBQPKDFVLONHNRISNLEBIFAKADEPW 180
DB 121 RSARGGQGTANDAAKALNNGSKQALDVKELAPRIVLHFNHINSLDKVFPVPAFY 180
QY 181 VPPFQVSSFTNVDEMEQW-ADNYFGTGDAAPDPDPVSIIVEGDSRTGKTMARALQPHN 239
DB 181 VPPFQVSSFTNVDEMEQW-ADNYFGTGDAAPDPDPVSIIVEGDSRTGKTMARALQPHN 239

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DB 181 VSPFLSSFPQVDELEHWSENVMDA--AAPWRPVSIIVEGDSRTGRTWARSLLQPHN 238
QY 240 YLSGHLDFNGRVPSNDVQVNVIDDIAPHYKLGMKMLLGAQDWMQNCYGVQIKG 299
DB 239 YLGGHLDLSQKYSNNAMVVIDVDPHY--LGHFKSEMGARQDWSNTYXKPIQIKG 296
QY 300 IPAIVLCNPEGASXYEFLDKAENTGAKNNTIKNAIFITLTAPLY-----QESTQASQETG 355
DB 297 IPIITFLCNPPQSSFKYLDLBEKNQALKNWATKATVITIHQPLFADLTONTISHRQEA 356
QY 356 NQ 357
DB 357 SR 358
XX
XX RESULT 13
XX ID AAR8871 standard; protein; 359 AA.
XX
XX AAR8871;
XX
XX 27-AUG-2003 (revised)
XX 07-NOV-1996 (first entry)
XX
XX Sardinian tomato yellow leaf curl virus mutated Rep protein (K227H).
XX
XX Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
XX modification; mutation; viral replication; deficient; inhibition;
XX viral resistance; geminivirus; tomato yellow leaf curl virus;
XX Sardinian isolate; STYLCV; transgenic plant; P-loop; C1 protein;
XX A11 protein.
XX
XX Tomato yellow leaf curl virus.
XX
XX Key Location/Qualifiers
XX Misc-difference 227
XX /note= "wild-type Lys has been replaced by His"
XX
XX WO9608573-A1.
XX
XX 21-MAR-1996.
XX
XX 15-SEP-1995; 95WO-FR001192.
XX
XX 15-SEP-1994; 94FR-00011040.
XX
XX (CNRS ) CENT NAT RECH SCI.
XX
XX Gronenborn B;
XX
XX WPI; 1996-179947/18.
XX
XX N-PSDB; AAT12905.
XX
XX Prodn. of virus-resistant transgenic plants - using mutated genomic
XX sequence from phytopathogenic DNA virus.
XX
XX Disclosure; Fig 13; 93pp; French.
XX
XX Mutation of consensus amino acids in the NTP-binding site of geminivirus
XX Rep protein is used to produce replication deficient viruses. The mutated
XX viral nucleic acid is used for producing transgenic plants that are
XX resistant to, or tolerant of, the native virus. The present sequence is a
XX mutant form of the Rep (or C1) protein from the Sardinian isolate of
XX tomato yellow leaf curl virus (STYLCV) in which the wild-type Lys227
XX residue has been changed to a His residue; transgenic Nicotiana
XX benthamiana plants generated by transformation with the mutated virus
XX were not resistant to STYLCV. In contrast, plants transformed with a
XX virus in which Lys227 had been replaced by Ala were found to be
XX resistant. (Updated on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 359 AA;
XX
Query Match 67.3%; Score 1305.5; DB 2; Length 359;

```

[illegible]

XX	AA88870		
XX	AA88870;		
DT	27-AUG-2003	(revised)	
DT	07-NOV-1996	(first entry)	
DE	Sardinian tomato yellow leaf curl virus mutated Rep protein (K227A)		
XX			
KW	Nucleotide triphosphate binding site; DNA helicase; RNA helicase;		
KM	modification; mutation; viral replication; deficiency; inhibition;		
KW	viral resistance; geminiviruses; tomato yellow leaf curl virus;		
KM	Sardinian isolate; STYLCV; transgenic plant; P-loop; C1 protein;		
KX	A11 protein; dominant negative phenotype.		
XX			
OS	Tomato yellow leaf curl virus.		
XX			
FH	Key	Location/Qualifiers	
FT	Misc-difference 227	/note= "wild-type Lys has been replaced by Ala"	
XX			
PN	MO9608573-Al.		
XX			
PD	21-MAR-1996.		
XX			
PF	15-SEP-1995;	95WO-FR001192.	
XX			
PR	15-SEP-1994;	94FR-00011040.	
XX			
PA	(CNRS) CENT NAT RECH SCT.		
XX			
PI	Gronenborn B;		
XX			
DR	WPI; 1996-179947/18.		
XX			
DR	N-PSDB; AAT12904.		
XX			
PT	Prodn. of virus-resistant transgenic plants - using mutated genomic		
XX	sequence from phytopathogenic DNA virus.		
XX			

PS	Disclosure; Fig 13; 93pp; French.
XX	
CC	Mutation of consensus amino acids in the NMP-binding site of geminivirus
CC	Rep protein is used to produce replication deficient viruses. The mutated
CC	viral nucleic acid is used for producing transgenic plants that are
CC	resistant to, or tolerant of, the native virus. The present sequence is a
CC	mutant form of the Rep (or CI) protein from the Sardinian isolate of
CC	tomato yellow leaf curl virus (STYLVCV) in which the wild-type lys227
CC	residue has been changed to an Ala residue; transgenic Nicotiana
CC	benthiana plants generated by transformation with the mutated virus
CC	were found to be resistant to STYLVCV, i.e. the mutation results in a
CC	dominant negative phenotype. (Updated on 27-AUG-2003 to correct OS
CC	field.)
CC	
CC	
CC	
SQ	Sequence 359 AA:
Query Match	67.3%; Score 1305.5; DB 2; Length 359;
Best Local Similarity	66.0%; Pred. No. 8e-113;
Matches 239;	Conservative 48; Mismatches 66; Indels 9; Gaps 4
OY	1 MPPEKKFRVOSKNYFLTYPOCSLSKERALSOLONANTPVNKKFTIKICRELTENGSEPHLAV 60
Dd	1 MPREGGRSIRAKNFYLYTPKCDLLKENALSGITMLQFPTNLFIKICRELHENGSEPHIHI 60
OY	61 LVDFEGKYQCTNNRFEDLVSPTRSAHFHPNIQGAKSSDVKSYYDKOGDTIEKGDPQIDG 120
Dd	61 LIQEGEKYNCTNQRFPLVSPTRSAHFHPNIQGAKSSDVKSYYDKOGDVLWEGTFQIDG 120
OY	121 RSAAGGGGSANDSAFAKALNGSVQSALAYLRBEPDPOFVLONHNIRSLERIFAKAPEPW 180
Dd	121 RSNAGGGGTATADAFYAKALNGSKQALDVLIELAPRDVLFHFNINSMLDKVFQVPAPPY 180
OY	181 VPPQVSSFTNVPPDEOMEN-ADNYFGTGDAAPPDRPVSIIYEGDSRTGKTMAARALGPHN 239
Dd	181 VSPFLSSPDQVPELEHMVSENWMDA--AAPPRPVSIVIEGDSRTGATTWARSILGPHN 238
OY	240 YLSHLDPNGRVFENDVQVYINVDIAHYLYLKTKMKELGAQXKMOSCKTGGKPQIQIGG 299
Dd	239 YLCCHLDLSQRYVSNMAMVNYVIDVDPHY--LKHFKEMGQRDMQSWTKYGKPIQIQIGG 296
OY	300 IPAIVLCNPGEAGSYKEFLDKAENTGKKNWTIKKAIFITTLAPPY----QESTQASQETG 355
Dd	297 IPTFLCNPGPOSFKRYLDBEKNQAALKMATKNAIFVTTHIQPLPADTNQNTTSRROBEA 356
OY	356 NQ 357
Dd	: :
Dd	357 SE 358
RESULT 15	
AAM34337	
ID	AAM34337 standard; protein; 357 AA.
AC	AAM34337;
XX	
XX	AA34337;
DT	17-OCT-2003 (revised)
DT	27-APR-1998 (first entry)
XX	
DE	Tomato yellow leaf curl virus CI protein.
XX	
KW	Geminivirus; TYLCV; C1 gene; transdominant mutation; transgenic plant;
OS	disease resistance.
XX	
OS	Tomato yellow leaf curl virus; strain Israel.
XX	
PN	MO9739110-Al.
PD	23-OCT-1997.
PF	15-APR-1997; 97MO-US006300.
PR	16-APR-1996; 96US-0015517P.
XX	

PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.
PA (MISC) WISCONSIN ALUMNI RES FOUND.

XX Stout UT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;
XX WPI; 1997-526447/48.

XX DR N-PSDB; AAT93311.

XX Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
PT genes - have increased resistance to geminivirus infection e.g. tomato
PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic
PT geminivirus.

XX Example 4.1; Page 80-81; 132pp; English.

CC This protein comprises the wild-type CI protein of tomato yellow leaf
CC curl virus (TYLCV), a geminivirus that has a monopartite genome. The CI
CC protein is required for replication. The invention involves production of
CC transgenic plants containing DNA comprising geminivirus AC1 or CI wild-
CC type or mutant sequences that negatively interfere in trans with
CC geminiviral replication during infection. Such transgenic plants are
CC resistant to viral infection. The AC1/CI genes are especially from TYLCV,
CC tomato mottle virus or bean golden mosaic geminivirus (see AAT93282-93)
CC and encode polypeptides (see AAW34324-35) that can have mutations in the
CC highly conserved DNA-nicking domain and/or the NTP-binding domain.
CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 357 AA;

Query Match 66.7%; Score 1293.5; DB 2; Length 357;

Best Local Similarity 66.3%; Pred. No. 1e-111;
Matches 238; Conservative 53; Mismatches 59; Indels 9; Gaps 4;

QY 4 PKKRVQSKNYFLTYPCQSLSKERALSOLOQNTLPVKKFKIKICRELHENGEPHLAVLQ 63
DB 2 PRLEFKIYAKNYFLTYPCQSLSKERALSOQLKLETPNKKYIKVCKELHENGEPHLAVLIQ 61
QY 64 FEGKYQCTNNRFFDLVSPTRSAHFHPNIOGAKSSDVKSYIDKGDITIEWGDFQIDGRSA 123
DB 62 FEGKYQCKNGRFFDLVSPNRSAHFHPNIOGAKSSDVKSYIDKGDITIEWGDFQIDGRSA 121
QY 124 RGGQOSANDSYAKALANGSVOSALAVREBOPKDFVLQNNHNRISNLERIFAKAPEPVPP 183
DB 122 RGGQOSANDSYAEALNGSISEALNIIKEKAPKDYIILQFNLSSNLDRIFFSPLEVYVSP 181
QY 184 FOVSFFTNVDEMEW-ADNYFGTGDAPPRPVSIIVEGDSRTGKTMARALGPHNYIS 242
DB 182 FLSSSFNQVPELSEWVAENV-VYSARPPRPISIVIEGDSRTGKTMARSLGPHNYLC 239
QY 243 GHLDENGRVPSNDVQVNVVIDIAPHYKLKMKELLAGQKDMQSNCKYKPFQIKGIPPA 302
DB 240 GHLDLSPKYSNDAMWNVVIDVNPY--LKHFKFIMAQRMQSNCKYKPFQIKGIPPT 297
QY 303 IVLGNBEGASYSKFFLDKAENTGLKNTTIKNAFITTLAPLY---QESTQASQETGNQ 357
DB 298 IFLCNPEPTSSYRRLDEKKNISLKNWALKNATFTVLEPFAFASINQPTQDSQETNKK 356

Search completed: December 3, 2004, 14:57:29
Job time: 159 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2004, 14:58:24 ; Search time 22 Seconds
(without alignments)
1088.218 Million cell updates/sec

Title: US-09-491-063a-2

Sequence: 1 MPPKKFRVQSKNYFLTYPO.....PLYQSTQASQETGNKAGG 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1908	98.4	361	3	US-08-838-151A-2
2	1902	98.1	361	3	US-08-838-151A-6
3	1892	97.6	361	3	US-08-838-151A-8
4	1886	97.3	361	3	US-08-838-151A-4
5	1572	81.1	353	3	US-08-838-151A-44
6	1572	81.1	353	3	US-08-838-151A-46
7	1567	80.8	353	3	US-08-838-151A-49
8	1566	80.8	353	3	US-08-838-151A-52
9	1564	80.7	353	3	US-08-838-151A-55
10	1311.5	67.6	359	3	US-08-809-103B-2
11	1308.5	67.5	359	3	US-08-809-103B-8
12	1305.5	67.3	359	3	US-08-809-103B-4
13	1305.5	66.7	357	3	US-08-809-103B-6
14	1293.5	66.7	357	3	US-08-838-151A-20
15	1293.5	66.7	357	3	US-08-838-151A-24
16	1290.5	66.6	357	3	US-08-838-151A-27
17	1288.5	66.5	357	3	US-08-838-151A-30
18	1288.5	66.1	34.1	3	US-08-838-151A-14
19	486	25.1	335	3	US-09-414-276-6
20	275.5	14.2	293	3	US-09-414-276-3
21	241	12.4	143	3	US-09-414-276-4
22	141	7.3	27	2	US-08-967-999-4
23	141	7.3	27	2	US-08-967-999-5
24	113	5.8	472	2	US-08-811-949-63
25	108	5.6	27	2	US-08-967-999-6
26	108	5.6	27	2	US-08-967-999-7
27	103.5	5.3	527	4	US-09-600-985-1

28	103.5	5.3	527	4	US-09-600-985-2	Sequence 2, Appl1
29	103.5	5.3	527	4	US-09-600-985-3	Sequence 3, Appl1
30	102.5	5.3	437	2	US-08-811-949-49	Sequence 49, Appl1
31	102.5	5.3	527	1	US-07-609-510B-16	Sequence 16, Appl1
32	102.5	5.3	527	4	US-09-612-314A-51	Sequence 51, Appl1
33	102.5	5.3	527	5	PCT-US91-01025A-2	Sequence 2, Appl1
34	102.5	5.3	527	6	5185259-8	Patent No. 5185259
35	102.5	5.3	562	2	US-08-811-949-43	Sequence 43, Appl1
36	102.5	5.3	562	2	US-08-560-098A-50	Sequence 50, Appl1
37	102.5	5.3	562	2	US-08-883-795A-38	Sequence 38, Appl1
38	102.5	5.3	562	4	US-09-703-695A-4	Sequence 4, Appl1
39	102.5	5.3	562	6	5185259-3	Patent No. 5185259
40	102.5	5.3	562	6	5200340-2	Patent No. 5200340
41	102.5	5.3	562	6	5344773-2	Patent No. 5344773
42	101.5	5.2	437	2	US-08-811-949-55	Sequence 55, Appl1
43	101.5	5.2	527	6	5520913-1	Patent No. 5520913
44	97	5.0	671	4	US-09-543-681A-5122	Sequence 5122, Ap
45	96	5.0	263	4	US-09-248-796A-23610	Sequence 23610, A

ALIGNMENTS

RESULT 1
US-08-838-151A-2
Sequence 2, Application US/0838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Lau, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Gemminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSER: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838, 151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-838-151A-2
Query Match 98.4%; Score 1908; DB 3; Length 361;
Best Local Similarity 98.3%; Pred. No. 2,5e-189;
Matches 355; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
1 MPPKKFRVQSKNYFLTYPOCSLSEKALSQLNTLPVKKFKIKICRELHNGEPHIAV 60
|||||

Db 1 MPPPKRRVQSKNYFLTYPCQSLSKERALSQLQNLNTPVKKFKICRELHENGEPHLHV 60
QY 61 LVQPEGKYQCTNNRFFDLVSPTRSAHFHPNIQAKSSSDVKSYYDKQDPTIEMGDFOIDG 120
Db 61 LVQPEGKYQCTNNRFFDLVSPTRSAHFHPNIQAKSSSDVKSYYDKQDPTIEMGDFOIDG 120
QY 121 RSARGGQGSANDSYAKALNAGSVQSAALAVIREOPKDFVLQNNHNRSLERIFAKABEPW 180
Db 121 RSARGGQGSANDSYAKALNAGSVQSAALAVIREOPKDFVLQNNHNRSLERIFAKABEPW 180
QY 181 VPPQVSSFTNVPEMOMADNYFGTGDAAAPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
Db 181 VPPQVSSFTNVPEMOMADNYFGTGDAAAPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
QY 241 LSGHLDNGRVSNDVQYNYIDIAAPHYLKTKMKKELGAKQKQMSCKTGKPVQIRGGI 300
Db 241 LSGHLDNGRVSNDVQYNYIDIAAPHYLKTKMKKELGAKQKQMSCKTGKPVQIRGGI 300
QY 301 PAIVLCNPGEGASKEFLDKAENTGLKNWTTIKNAIFITLTAPLYQDSTQASQETGNOQAK 360
Db 301 PAIVLCNPGEGASKEFLDKAENTGLKNWTTIKNAIFITLTAPLYQDSTQASQETGNOQAK 360
QY 361 G 361
Db 361 G 361

RESULT 2

US-08-838-151A-6
; Sequence 6, Application US/08838151A
; Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlgvist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milanow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838.151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-6

Query Match 98.1%; Score 1902; DB 3; Length 361;
Best Local Similarity 98.1%; Pred. No. 1e-188;

Matches 354; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 MPPPKRRVQSKNYFLTYPCQSLSKERALSQLQNLNTPVKKFKICRELHENGEPHLHV 60
Db 1 MPPPKRRVQSKNYFLTYPCQSLSKERALSQLQNLNTPVKKFKICRELHENGEPHLHV 60
QY 61 LVQPEGKYQCTNNRFFDLVSPTRSAHFHPNIQAKSSSDVKSYYDKQDPTIEMGDFOIDG 120
Db 61 LVQPEGKYQCTNNRFFDLVSPTRSAHFHPNIQAKSSSDVKSYYDKQDPTIEMGDFOIDG 120
QY 121 RSARGGQGSANDSYAKALNAGSVQSAALAVIREOPKDFVLQNNHNRSLERIFAKABEPW 180
Db 121 RSARGGQGSANDSYAKALNAGSVQSAALAVIREOPKDFVLQNNHNRSLERIFAKABEPW 180
QY 181 VPPQVSSFTNVPEMOMADNYFGTGDAAAPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
Db 181 VPPQVSSFTNVPEMOMADNYFGTGDAAAPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
QY 241 LSGHLDNGRVSNDVQYNYIDIAAPHYLKTKMKKELGAKQKQMSCKTGKPVQIRGGI 300
Db 241 LSGHLDNGRVSNDVQYNYIDIAAPHYLKTKMKKELGAKQKQMSCKTGKPVQIRGGI 300
QY 301 PAIVLCNPGEGASKEFLDKAENTGLKNWTTIKNAIFITLTAPLYQDSTQASQETGNOQAK 360
Db 301 PAIVLCNPGEGASKEFLDKAENTGLKNWTTIKNAIFITLTAPLYQDSTQASQETGNOQAK 360
QY 361 G 361
Db 361 G 361

RESULT 3

US-08-838-151A-8
; Sequence 8, Application US/08838151A
; Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlgvist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milanow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838.151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-838-151A-8

Query Match 97.6%; Score 1892; DB 3; Length 361;
Best Local Similarity 97.8%; Pred. No. 1,1e-187;
Matches 353; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MPPPKRRVSKYVFLTYPCSSLSKEALSQLNLNTPVKKFKIKICREIHENGEPHLAV 60
DB 1 MPPPKRRVSKYVFLTYPCSSLSKEALSQLNLNTPVKKFKIKICREIHENGEPHLAV 60
QY 61 LVPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVKSYIDKDGDTIEWGDFQIDG 120
DB 61 LVPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVKSYIDKDGDTIEWGDFQIDG 120
QY 121 RSARGGQOSANDSYAKALNMGVQSALAVLREOPKDFVLQNNHINSNLERIFAKAPEPW 180
DB 121 RSARGGQOSANDSYAKALNMGVQSALAVLREOPKDFVLQNNHINSNLERIFAKAPEPW 180
QY 181 VPPFOVSSFTNVPEDEMADNFTGDAAPDPSPVSIIVEGDSRTGKTMMABALGPHNY 240
DB 181 VPPFOVSSFTNVPEDEMADNFTGDAAPDPSPVSIIVEGDSRTGKTMMABALGPHNY 240
QY 241 LSGHLDNNGRVFNSDVQYNNVIDIAPHYLKLGKMKELGAKQKQWQSNCKYKGPVQIKGI 300
DB 241 LSGHLDNNGRVFNSDVQYNNVIDIAPHYLKLGKMKELGAKQKQWQSNCKYKGPVQIKGI 300
QY 301 PAIVLCNPGGASKEYFLDKAENTGLKNWTIKNAIFITLTPALYQDSTQASQETGNQKQ 360
DB 301 PAIVLCNPGGASKEYFLDKAENTGLKNWTIKNAIFITLTPALYQDSTQASQETGNQKQ 360
QY 361 G 361
DB 361 G 361

RESULT 4

US-08-838-151A-4
Sequence 4, Application US/08838151A

Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-4

Query Match 97.3%; Score 1886; DB 3; Length 361;
Best Local Similarity 97.5%; Pred. No. 4.7e-187;
Matches 352; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 MPPPKRRVSKYVFLTYPCSSLSKEALSQLNLNTPVKKFKIKICREIHENGEPHLAV 60
DB 1 MPPPKRRVSKYVFLTYPCSSLSKEALSQLNLNTPVKKFKIKICREIHENGEPHLAV 60
QY 61 LVPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVKSYIDKDGDTIEWGDFQIDG 120
DB 61 LVPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVKSYIDKDGDTIEWGDFQIDG 120
QY 121 RSARGGQOSANDSYAKALNMGVQSALAVLREOPKDFVLQNNHINSNLERIFAKAPEPW 180
DB 121 RSARGGQOSANDSYAKALNMGVQSALAVLREOPKDFVLQNNHINSNLERIFAKAPEPW 180
QY 181 VPPFOVSSFTNVPEDEMADNFTGDAAPDPSPVSIIVEGDSRTGKTMMABALGPHNY 240
DB 181 VPPFOVSSFTNVPEDEMADNFTGDAAPDPSPVSIIVEGDSRTGKTMMABALGPHNY 240
QY 241 LSGHLDNNGRVFNSDVQYNNVIDIAPHYLKLGKMKELGAKQKQWQSNCKYKGPVQIKGI 300
DB 241 LSGHLDNNGRVFNSDVQYNNVIDIAPHYLKLGKMKELGAKQKQWQSNCKYKGPVQIKGI 300
QY 301 PAIVLCNPGGASKEYFLDKAENTGLKNWTIKNAIFITLTPALYQDSTQASQETGNQKQ 360
DB 301 PAIVLCNPGGASKEYFLDKAENTGLKNWTIKNAIFITLTPALYQDSTQASQETGNQKQ 360
QY 361 G 361
DB 361 G 361

RESULT 5

US-08-838-151A-44
Sequence 44, Application US/08838151A

Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-44

Query Match 81.1%; Score 1572; DB 3; Length 353;
Best Local Similarity 80.4%; Pred. No. 1.8e-154;
Matches 283; Conservative 31; Mismatches 38; Indels 0; Gaps 0;

QY 1 MPPPKRRVSKNYFLTYPCQSLSKERALSQLQNLNPNVKKFKIKICREIHENGEPLHAY 60
DB 1 MPPQRRVSKNYFLTYPCPIPKKEVLSQLQKHITATNKKFKICEEHEENGEPLHA 60
QY 61 LVPEGKYQCTNNRFFDLVSPTRSAHPHNPNOGAKSSSDVKSYYIDKDGDTIEMGDFQIDG 120
DB 61 LIQEGKFVCTNKRFLPLVSTSRAPHPHNPNOGAKSSSDVKAVIDKDGVTIEMGDFQYDG 120
QY 121 RSARGGQGSANDSYAKALNAGVQALAVLREOPKDFVLQNHINIRSNLERIFAKADEPW 180
DB 121 RSARGGQGSANDSYAKALNADSIRESALTILKEQPKDYVLQHNIRSNLERIFVKYDEPW 180
QY 181 VPPQVSSFTNVPEDEMOMADNYFGTGDAPRDRPVSIIEGDSRTGKTMMARALGPHNY 240
DB 181 VPPPLSSFTNVPMQEWDDYFGRSAPRPERPISIIIEGDSRTGKTMMARALGPHNY 240
QY 241 LSGHLDENGWVFSNDVQYNNVIDIAPHYLKLKMKKELGAKQWQSNCKYKGPVQIKGI 300
DB 241 LSGHLDENSNVYNAAYNNVIDISPNYLLKMKKELGAKQWQSNCKYKGPVQIKGI 300
QY 301 PAIVLCNPGGASGYKEFLDKAENTGLKNWTTIKNAIFITTLAPLYQSTQASQ 352
DB 301 PSIVLCNPGGSSYKDFLDKEENRALHNTIHNALFVTLTAPLYQSTTQDCQ 352

RESULT 6

US-08-838-151A-46
Sequence 46, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-46

Query Match 81.1%; Score 1572; DB 3; Length 353;
Best Local Similarity 80.4%; Pred. No. 1.8e-154;
Matches 283; Conservative 31; Mismatches 38; Indels 0; Gaps 0;

QY 1 MPPPKRRVSKNYFLTYPCQSLSKERALSQLQNLNPNVKKFKIKICREIHENGEPLHAY 60
DB 1 MPPQRRVSKNYFLTYPCPIPKKEVLSQLQKHITATNKKFKICEEHEENGEPLHA 60
QY 61 LVPEGKYQCTNNRFFDLVSPTRSAHPHNPNOGAKSSSDVKSYYIDKDGDTIEMGDFQIDG 120
DB 61 LIQEGKFVCTNKRFLPLVSTSRAPHPHNPNOGAKSSSDVKAVIDKDGVTIEMGDFQYDG 120
QY 121 RSARGGQGSANDSYAKALNAGVQALAVLREOPKDFVLQNHINIRSNLERIFAKADEPW 180
DB 121 RSARGGQGSANDSYAKALNADSIRESALTILKEQPKDYVLQHNIRSNLERIFVKYDEPW 180
QY 181 VPPQVSSFTNVPEDEMOMADNYFGTGDAPRDRPVSIIEGDSRTGKTMMARALGPHNY 240
DB 181 VPPPLSSFTNVPMQEWDDYFGRSAPRPERPISIIIEGDSRTGKTMMARALGPHNY 240
QY 241 LSGHLDENGWVFSNDVQYNNVIDIAPHYLKLKMKKELGAKQWQSNCKYKGPVQIKGI 300
DB 241 LSGHLDENSNVYNAAYNNVIDISPNYLLKMKKELGAKQWQSNCKYKGPVQIKGI 300
QY 301 PAIVLCNPGGASGYKEFLDKAENTGLKNWTTIKNAIFITTLAPLYQSTQASQ 352
DB 301 PSIVLCNPGGSSYKDFLDKEENRALHNTIHNALFVTLTAPLYQSTTQDCQ 352

RESULT 7

US-08-838-151A-49
Sequence 49, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-49

Query Match 80.8%; Score 1567; DB 3; Length 353;
Best Local Similarity 80.1%; Pred. No. 6e-154;
Matches 282; Conservative 31; Mismatches 39; Indels 0; Gaps 0;

```
QY 1 MPPPKFRVQSKNYFLTYPCQSLSKERALSQLQNLNTPVKKFKIKICREIHENGEPHLAV 60
DB 1 MPPPKFRVQSKNYFLTYPCQSLSKERALSQLQNLNTPVKKFKIKICREIHENGEPHLA 60
QY 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSSDVKSYYDKDGTIEMGDPIQIDG 120
DB 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSSDVKSYYDKDGTIEMGDPIQIDG 120
QY 121 RSARGGQOSANDSYAKALNAGVOSALAVAREOPKDFVLQNHINIRSNLERIFAKAPEPW 180
DB 121 RSARGGQOSANDSYAKALNAGVOSALAVAREOPKDFVLQNHINIRSNLERIFAKAPEPW 180
QY 181 VPPFOVSSFTNVDEMOMADNYFGTDAAPDDRVSIIIEGDSRTGKTWABALGPHNY 240
DB 181 VPPFOVSSFTNVDEMOMADNYFGTDAAPDDRVSIIIEGDSRTGKTWABALGPHNY 240
QY 241 LSGHLDPNHGVFNVDQVNYIDIAPIHYLKLKMKWELGAKQWQSNCKYKPKVQIKGI 300
DB 241 LSGHLDPNHGVFNVDQVNYIDIAPIHYLKLKMKWELGAKQWQSNCKYKPKVQIKGI 300
QY 301 PATVLCNPGSGASYKEFLDKAENTGLKNMTIKKAIPTLTAPLYQSTQASQ 352
DB 301 PATVLCNPGSGASYKEFLDKAENTGLKNMTIKKAIPTLTAPLYQSTQASQ 352
```

RESULT 8

US-08-838-151A-52
Sequence 52, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-52

Query Match 80.8%; Score 1566; DB 3; Length 353;
Best Local Similarity 80.1%; Pred. No. 7.6e-154;
Matches 282; Conservative 31; Mismatches 39; Indels 0; Gaps 0;

```
QY 1 MPPPKFRVQSKNYFLTYPCQSLSKERALSQLQNLNTPVKKFKIKICREIHENGEPHLAV 60
DB 1 MPPPKFRVQSKNYFLTYPCQSLSKERALSQLQNLNTPVKKFKIKICREIHENGEPHLA 60
QY 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSSDVKSYYDKDGTIEMGDPIQIDG 120
DB 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSSDVKSYYDKDGTIEMGDPIQIDG 120
QY 121 RSARGGQOSANDSYAKALNAGVOSALAVAREOPKDFVLQNHINIRSNLERIFAKAPEPW 180
DB 121 RSARGGQOSANDSYAKALNAGVOSALAVAREOPKDFVLQNHINIRSNLERIFAKAPEPW 180
QY 181 VPPFOVSSFTNVDEMOMADNYFGTDAAPDDRVSIIIEGDSRTGKTWABALGPHNY 240
DB 181 VPPFOVSSFTNVDEMOMADNYFGTDAAPDDRVSIIIEGDSRTGKTWABALGPHNY 240
QY 241 LSGHLDPNHGVFNVDQVNYIDIAPIHYLKLKMKWELGAKQWQSNCKYKPKVQIKGI 300
DB 241 LSGHLDPNHGVFNVDQVNYIDIAPIHYLKLKMKWELGAKQWQSNCKYKPKVQIKGI 300
QY 301 PATVLCNPGSGASYKEFLDKAENTGLKNMTIKKAIPTLTAPLYQSTQASQ 352
DB 301 PATVLCNPGSGASYKEFLDKAENTGLKNMTIKKAIPTLTAPLYQSTQASQ 352
```

RESULT 9

US-08-838-151A-55
Sequence 55, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-55

Query Match 80.7%; Score 1564; DB 3; Length 353;
Best Local Similarity 80.1%; Pred. No. 1,2e-153;
Matches 282; Conservative 31; Mismatches 39; Indels 0; Gaps 0;

QY 1 MPPPKRRVQSKYFLTYPCQSLSKERALSQLQNLNTPVAKKFKIKRELHENGEPHLAV 60
DB 1 MPPQRRVQSKYFLTYPCQSLSKERALSQLQNLNTPVAKKFKIKRELHENGEPHLA 60
QY 61 LVQEGKYQCTNNRFPDLVSPTRSAHFHPIIQAKSSDVKSYIDKDGDTIEMGDFQIDG 120
DB 61 LIQEGKFVCTNKRFLPLVSTRSAPFHPIIQAKSSDVKAYIDKDGVTIEMGQFQYDG 120
QY 121 RSARGGQOSANDSYAKALNAGSVQALAVLREOPKDFVLQNHNRSLERIFAKAPEPW 180
DB 121 RSARGGQOSANDSYAKALNAGSVQALAVLREOPKDFVLQNHNRSLERIFAKAPEPW 180
QY 181 VPPFOVSSFTNVPEDEMOMADNYFTGDAAPDRPVSIIVEGDSRTGKTMMARALGFPHN 240
DB 181 VPPPLSSFTNVPEDEMOMADNYFTGDAAPDRPVSIIVEGDSRTGKTMMARALGFPHN 240
QY 241 LSGHLDNGRVSNDVQYVNDIAPHYLKLKMKKELGAQDWQSNCKRYGPVQIKG 300
DB 241 LSGHLDNSKRVSNVAVYVNDIAPHYLKLKMKKELGAQDWQSNCKRYGPVQIKG 300
QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKMTIKNAIFITLTAPLYQESTQASQ 352
DB 301 PSIVLCNPGEGASYKDFLDKENTGLKMTIKNAIFITLTAPLYQESTQDQ 352

RESULT 10
US-08-809-103B-2
Sequence 2, Application US/08809103B
Patent No. 6133505
GENERAL INFORMATION:
APPLICANT: GROENBORN, Bruno
TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS FOR OBTAINING SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925

REFERENCE/DOCKET NUMBER: US994AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-103B-2

Query Match 67.6%; Score 1311.5; DB 3; Length 359;
Best Local Similarity 66.3%; Pred. No. 2.1e-127;
Matches 240; Conservative 48; Mismatches 65; Indels 9; Gaps 4;

QY 1 MPPPKRRVQSKYFLTYPCQSLSKERALSQLQNLNTPVAKKFKIKRELHENGEPHLAV 60
DB 1 MPPSGRFSIRAKYFLTYPCQSLSKERALSQLQNLNTPVAKKFKIKRELHENGEPHLA 60
QY 61 LVQEGKYQCTNNRFPDLVSPTRSAHFHPIIQAKSSDVKSYIDKDGDTIEMGDFQIDG 120
DB 61 LIQEGKFVCTNKRFLPLVSTRSAPFHPIIQAKSSDVKSYIDKDGDTIEMGQFQYDG 120
QY 121 RSARGGQOSANDSYAKALNAGSVQALAVLREOPKDFVLQNHNRSLERIFAKAPEPW 180
DB 121 RSARGGQOSANDSYAKALNAGSVQALAVLREOPKDFVLQNHNRSLERIFAKAPEPW 180
QY 181 VPPFOVSSFTNVPEDEMOMADNYFTGDAAPDRPVSIIVEGDSRTGKTMMARALGFPHN 239
DB 181 VPPPLSSFTNVPEDEMOMADNYFTGDAAPDRPVSIIVEGDSRTGKTMMARALGFPHN 238
QY 240 YLSGHDNGRVSNDVQYVNDIAPHYLKLKMKKELGAQDWQSNCKRYGPVQIKG 299
DB 240 YLSGHDNSKRVSNVAVYVNDIAPHYLKLKMKKELGAQDWQSNCKRYGPVQIKG 296
QY 300 IPAIVLCNPGEGASYKEFLDKAENTGLKMTIKNAIFITLTAPLYQESTQASQ 355
DB 300 IPVILCNPGEGASYKEFLDKAENTGLKMTIKNAIFITLTAPLYQESTQDQ 356
QY 356 NO 357
DB 357 SE 358

RESULT 11
US-08-809-103B-8
Sequence 8, Application US/08809103B
Patent No. 6133505
GENERAL INFORMATION:
APPLICANT: GROENBORN, Bruno
TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS FOR OBTAINING SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040

FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-103B-8

Query Match 67.5%; Score 1308.5; DB 3; Length 359;
Best Local Similarity 66.0%; Pred. No. 4,2e-127;
Matches 239; Conservative 49; Mismatches 65; Indels 9; Gaps 4;

QY 1 MPPPKKRVQSKNYFLTYPCQSLSKKEALSQLQNLTPVKKFKIKICRELHENGEPHLAV 60
DB 1 MPSSGRFSIAKAKYFLTYPCDLTKENALSQLQNLTPVKKFKIKICRELHENGEPHLAI 60
QY 61 LVQFEGKYCTNNRFPDLVSPTRSAHFPHNIQAKSSDVSKSYIDKDGDTIEKDPQIDG 120
DB 61 LIQFEGKYCTNNRFPDLVSPTRSAHFPHNIQAKSSDVSKSYIDKDGDTIEKDPQIDG 120
QY 121 RSARGGQGSANDSYAKALNAGVSQALAVLREOPKDFVLQNHNTIRSNLERIFAKAPEPW 180
DB 121 RSARGGQGSANDSYAKALNAGVSQALAVLREOPKDFVLQNHNTIRSNLERIFAKAPEPW 180
QY 121 RSARGGQGSANDSYAKALNAGVSQALAVLREOPKDFVLQNHNTIRSNLERIFAKAPEPW 180
DB 121 RSARGGQGSANDSYAKALNAGVSQALAVLREOPKDFVLQNHNTIRSNLERIFAKAPEPW 180
QY 181 VPPFQVSSFTNVPDMEQEW-ADNYFGTGDAPDRPVSIIVEGDSRTGKTMMARALGPHN 239
DB 181 VPPFQVSSFTNVPDMEQEW-ADNYFGTGDAPDRPVSIIVEGDSRTGKTMMARALGPHN 239
QY 240 YLSGHLDFNGRVPSNDVQVNVIDDIAPHYLKLMKMKELGAQKQWQSNCKYKGPVQIKGG 299
DB 239 YLSGHLDFNGRVPSNDVQVNVIDDIAPHYLKLMKMKELGAQKQWQSNCKYKGPVQIKGG 299
QY 300 IPALVLCNPGEGASKEFLDKAENTGLKNWTIKNAIFITLTAPLY-----QESTQASQETG 355
DB 297 IPALVLCNPGEGASKEFLDKAENTGLKNWTIKNAIFITLTAPLY-----QESTQASQETG 355
QY 356 NQ 357
DB 357 SE 358

RESULT 12
US-08-809-103B-4
Sequence 4, Application US/08809103B
Patent No. 6133505
GENERAL INFORMATION:
APPLICANT: GRONENBORN, Bruno
TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-103B-4

Query Match 67.3%; Score 1305.5; DB 3; Length 359;
Best Local Similarity 66.0%; Pred. No. 8.6e-127;
Matches 239; Conservative 48; Mismatches 66; Indels 9; Gaps 4;

QY 1 MPPPKKRVQSKNYFLTYPCQSLSKKEALSQLQNLTPVKKFKIKICRELHENGEPHLAV 60
DB 1 MPSSGRFSIAKAKYFLTYPCDLTKENALSQLQNLTPVKKFKIKICRELHENGEPHLAI 60
QY 61 LVQFEGKYCTNNRFPDLVSPTRSAHFPHNIQAKSSDVSKSYIDKDGDTIEKDPQIDG 120
DB 61 LIQFEGKYCTNNRFPDLVSPTRSAHFPHNIQAKSSDVSKSYIDKDGDTIEKDPQIDG 120
QY 121 RSARGGQGSANDSYAKALNAGVSQALAVLREOPKDFVLQNHNTIRSNLERIFAKAPEPW 180
DB 121 RSARGGQGSANDSYAKALNAGVSQALAVLREOPKDFVLQNHNTIRSNLERIFAKAPEPW 180
QY 181 VPPFQVSSFTNVPDMEQEW-ADNYFGTGDAPDRPVSIIVEGDSRTGKTMMARALGPHN 239
DB 181 VPPFQVSSFTNVPDMEQEW-ADNYFGTGDAPDRPVSIIVEGDSRTGKTMMARALGPHN 239
QY 240 YLSGHLDFNGRVPSNDVQVNVIDDIAPHYLKLMKMKELGAQKQWQSNCKYKGPVQIKGG 299
DB 239 YLSGHLDFNGRVPSNDVQVNVIDDIAPHYLKLMKMKELGAQKQWQSNCKYKGPVQIKGG 299
QY 300 IPALVLCNPGEGASKEFLDKAENTGLKNWTIKNAIFITLTAPLY-----QESTQASQETG 355
DB 297 IPALVLCNPGEGASKEFLDKAENTGLKNWTIKNAIFITLTAPLY-----QESTQASQETG 355
QY 356 NQ 357
DB 357 SE 358

RESULT 13
US-08-809-103B-6
Sequence 6, Application US/08809103B
Patent No. 6133505
GENERAL INFORMATION:
APPLICANT: GRONENBORN, Bruno
TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington

```

STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-103B-6

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```

Query Match 67.3%; Score 1305.5; DB 3; Length 359;
Best Local Similarity 66.0%; Pred. No. 8.6e-127;
Matches 239; Conservative 48; Mismatches 66; Indels 9; Gaps 4;

QY 1 MPPKKFVOSKNYFLTYPOCSLSKEBALSQLONTLPVKKFKIKREIHENGEPHLHY 60
DB 1 MPRGRSRISAKNYFLTYPKCDLTKEBALSQLONTLPVKKFKIKREIHENGEPHLHY 60
QY 61 LVQEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSSDVKSITDKDGTIEMGDFOIDG 120
DB 61 LIQEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSSDVKSITDKDGTIEMGDFOIDG 120
QY 121 RASAGGQOSANDSYAKALNAGSVOSALAVLREBPQKDFVLONHNIRSNLERIPAKAPEPW 180
DB 121 RASAGGQOTANDAYAKALNAGSKQALDVIKELAPRDVLFHFNHINSNLDKVFVPPAPY 180
QY 181 VPPQVSSFTNVPEMDEM-ADNYFGTGDAAPDRPVSIIVEGDSRTGKTMMARALGPHN 239
DB 181 VSPFLSSFFDQVPELEHVENWMDA--AAKPRPVSIVIEGDSRTGKTMMARALGPHN 239
QY 240 YLSGHLDFNGRVSNDVOYVNIIDIAPHYTLKIMKELLGAQKQWQNSCKYKGPVQIKG 299
DB 239 YLCGLDLISQKVSNNMAYNVIDVDPHY--LKHFKEPMGAQRDWSQTKYKGIQIKG 296
QY 300 IPAIVLCNPGEGASYKEFLDKAENTGKKNWITKNAIFITLTAPLY---QESTQASQETG 355
DB 297 IPTFLCNPGQSSFFKEYLDEKQKQALKNMATKNAIFVITIQPLFADTNTTSHROEA 356
QY 356 NO 357
DB 357 SE 358

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RESULT 14
US-08-838-151A-20
Sequence 20, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T

```

```

APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESS: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-20

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Query Match 66.7%; Score 1293.5; DB 3; Length 357;
Best Local Similarity 66.3%; Pred. No. 1.5e-125;
Matches 238; Conservative 53; Mismatches 59; Indels 9; Gaps 4;

QY 4 PKKRVOSKNYFLTYPOCSLSKEBALSQLONTLPVKKFKIKREIHENGEPHLHY 63
DB 2 PRLFKIYAKNYFLTYPCSLSKKEBALSQLKLEFPTNKVITKYCKELHENGEPHLHY 61
QY 64 PEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSSDVKSITDKDGTIEMGDFOIDG 123
DB 62 PEGKYQCKNRFPLVSPNRSAPHFHPNIQAKSSTDVKTVEKDGNEFIDGVSQIDG 121
QY 124 RGGQOSANDSYAKALNAGSVOSALAVLREBPQKDFVLONHNIRSNLERIPAKAPEPW 183
DB 122 RGGQOSANDYAEALNAGSISEBALNIEKAPDYIIFQNLSSNDRITSPLEVYVSP 181
QY 184 FOVSFTNVPEMDEM-ADNYFGTGDAAPDRPVSIIVEGDSRTGKTMMARALGPHN 242
DB 182 FLSSFFQVDELEWVAENV--VYSAAPRPRISIVIEGDSRTGKTMMARALGPHN 239
QY 243 GHDPKRVVSNDVOYVNIIDIAPHYTLKIMKELLGAQKQWQNSCKYKGPVQIKG 302
DB 240 GHLDLSPKVSNDMAYNVIDVDPHY--LKHFKEPMGAQRDWSQTKYKGIQIKG 297
QY 303 IYLCNPGEGASYKEFLDKAENTGKKNWITKNAIFITLTAPLY---QESTQASQETG 357
DB 298 IFLCNPGFTSYREYLDKKNISLKNMALKNATFVITLYEPLFASINQPTQDSQETNK 356

```

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RESULT 15
US-08-838-151A-24
Sequence 24, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T

```


APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing GeminiViruses
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-24

Query Match 66.7%; Score 1293.5; DB 3; Length 357;
Best Local Similarity 66.3%; Pred. No. 1.5e-125;
Matches 238; Conservative 53; Mismatches 59; Indels 9; Gaps 4;

QY 4 PKKFRVQSKNYFTYPOCSLSKEBALSQLONTVPNNKFIKICRELEHNGEPHLYLVQ 63
DB 2 PRLFKIYAKNYFLTYPCSLSKKEBALSQLKLETPNNKYIKVCKELHNGEBPHLYLIQ 61
QY 64 FEKGYOCTNNRFPDIVSPTSAHFPPIQAKSSSDVKSYYIDKGDPTIEMGDFOIDGRSA 123
DB 62 FEKGYOCTNNRFPDLVSPNRSAPHPNIOAKSSTDVKTVERDGNFIDGVSQIDGRSA 121
QY 124 RGGQOSANDSYAKALNAGVOSALAVLREBQPKDFVLQNNHINSNLERIPAKAPEPVPP 183
DB 122 RGGQOSANDYAAALNAGSGSEALNLIKAKPKDYILQFNLSNLDRIIPPLEVYVSP 181
QY 184 FOVSSTFNVDENQEW-ADNYFGTGAAPDRPVSIIVEGDSRTGKTMARALGPHNYLS 242
DB 182 FLSSSFNQYVDELEEWAEENV--VYSAPRPWRPISIVIEGDSRTGKTMARSLGPHNYLC 239
QY 243 GHLDFFNGRVSNQVNVVIDIAPHYLKHKWELLGAOKWQSNCKYKGPVOIKGSIIPA 302
DB 240 GHLDLSPKVSNDAMVIVDDVDPHY--LKHFKFPGAGQDWQSNTRYGKPIQKGIPT 297
QY 303 IVLNPGEGASVKEFLDKAENTGKKNWTIKNAIFITLTAPLY---QESTOASQETGNQ 357
DB 298 IFLCNPGPTSSYREYDEBKNTISLKNWALKNATFTVLTLYEPFLPASINGPTQDSQETNK 356

Search completed: December 3, 2004, 15:02:11
Job time: 24 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2004, 15:02:15 ; Search time 144 Seconds
(without alignments)
894.034 Million cell updates/sec

Title: US-09-491-063a-2

Sequence: 1 MPPPKFRVQSKNYFLTPQ.....PLYQSTQASQETGNQAG 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1908	98.4	361	US-08-838-151A-2	Sequence 2, Appl1
2	1902	98.1	361	US-08-838-151A-6	Sequence 6, Appl1
3	1892	97.6	361	US-08-838-151A-8	Sequence 8, Appl1
4	1886	97.3	361	US-08-838-151A-4	Sequence 4, Appl1
5	1572	81.1	353	US-08-838-151A-46	Sequence 44, Appl1
6	1572	81.1	353	US-08-838-151A-45	Sequence 46, Appl1
7	1567	80.8	353	US-08-838-151A-49	Sequence 49, Appl1
8	1566	80.8	353	US-08-838-151A-52	Sequence 52, Appl1
9	1564	80.7	353	US-08-838-151A-55	Sequence 55, Appl1
10	1504.5	77.6	352	US-10-633-850-80	Sequence 80, Appl1
11	1503.5	77.5	352	US-10-633-850-84	Sequence 84, Appl1
12	1502.5	77.5	352	US-10-633-850-1	Sequence 1, Appl1
13	1502.5	77.5	352	US-10-633-850-64	Sequence 64, Appl1

14	1500.5	77.4	352	US-10-633-850-86	Sequence 86, Appl1
15	1499.5	77.3	352	US-10-633-850-82	Sequence 82, Appl1
16	1499.5	77.3	352	US-10-633-850-92	Sequence 92, Appl1
17	1499.5	77.3	352	US-10-633-850-94	Sequence 94, Appl1
18	1499	77.3	356	US-09-289-346A-11	Sequence 11, Appl1
19	1497.5	77.2	352	US-10-633-850-90	Sequence 90, Appl1
20	1496.5	77.2	352	US-10-633-850-58	Sequence 58, Appl1
21	1496.5	77.2	352	US-10-633-850-88	Sequence 88, Appl1
22	1496.5	77.2	352	US-10-633-850-98	Sequence 98, Appl1
23	1495.5	77.1	352	US-10-633-850-76	Sequence 76, Appl1
24	1494.5	77.1	352	US-10-633-850-68	Sequence 68, Appl1
25	1494.5	77.1	352	US-10-633-850-96	Sequence 96, Appl1
26	1492.5	77.0	352	US-10-633-850-62	Sequence 62, Appl1
27	1492.5	77.0	352	US-10-633-850-78	Sequence 78, Appl1
28	1490.5	76.9	352	US-10-633-850-74	Sequence 74, Appl1
29	1488.5	76.8	352	US-10-633-850-52	Sequence 52, Appl1
30	1488.5	76.8	352	US-10-633-850-66	Sequence 66, Appl1
31	1487.5	76.7	352	US-10-633-850-56	Sequence 56, Appl1
32	1486.5	76.7	352	US-10-633-850-60	Sequence 60, Appl1
33	1485.5	76.6	352	US-10-633-850-72	Sequence 72, Appl1
34	1480.5	76.4	352	US-10-633-850-54	Sequence 54, Appl1
35	1478.5	76.3	352	US-10-633-850-70	Sequence 70, Appl1
36	1293.5	66.7	357	US-08-838-151A-20	Sequence 20, Appl1
37	1293.5	66.7	357	US-08-838-151A-24	Sequence 24, Appl1
38	1290.5	66.6	357	US-08-838-151A-30	Sequence 30, Appl1
39	1288.5	66.5	357	US-08-838-151A-107	Sequence 107, Appl1
40	1230.5	63.5	349	US-10-633-850-112	Sequence 112, Appl1
41	1225.5	63.2	349	US-10-633-850-114	Sequence 114, Appl1
42	661	34.1	131	US-08-838-151A-14	Sequence 14, Appl1
43	486	25.1	335	US-10-151-336-6	Sequence 3, Appl1
44	275.5	14.2	293	US-10-151-336-3	Sequence 602, Appl1
45	257	13.3	264	US-10-310-154-602	

ALIGNMENTS

RESULT 1
US-08-838-151A-2
; Sequence 2, Application US/08838151A
; Publication No. US20010011379A1
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing GeminiViruses
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; City: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-2

Query Match 98.4%; Score 1908; DB 8; Length 361;
Best Local Similarity 98.3%; Pred. No. 1,1e-162;
Matches 355; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPPPKFRVOSKNYFLTYPOCSLSKEBALSQLONTLPVKKFKIKICREIHENGEPHLAV 60
DB 1 MPPPKFRVOSKNYFLTYPOCSLSKEBALSQLONTLPVKKFKIKICREIHENGEPHLAV 60
QY 61 LVQPEGKYQCTNNRFPDLVSPTRSAHPHPIQAKSSSDVKSVIDKDGDTIEWGDFQIDG 120
DB 61 LVQPEGKYQCTNNRFPDLVSPTRSAHPHPIQAKSSSDVKSVIDKDGDTIEWGDFQIDG 120
QY 121 RSARGGQGSANDSYAKALNAGSVOSALAVLREOPKDFVLQNNHRSNLERIFAKAPEPW 180
DB 121 RSARGGQGSANDSYAKALNAGSVOSALAVLREOPKDFVLQNNHRSNLERIFAKAPEPW 180
QY 181 VPPFOVSSFTNVDEMOMADNYFGTGDAAPDRPVSIIEGDSRTGKTMAALGPHNY 240
DB 181 VPPFOVSSFTNVDEMOMADNYFGTGDAAPDRPVSIIEGDSRTGKTMAALGPHNY 240
QY 241 LSGHLDNFGVPSNDVOYNYIDIAPIHYLKLKMKELGAKOMQSNCKYKGPVQIKGI 300
DB 241 LSGHLDNFGVPSNDVOYNYIDIAPIHYLKLKMKELGAKOMQSNCKYKGPVQIKGI 300
QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQSTQASQETGNQAK 360
DB 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQSTQASQETGNQAK 360
QY 361 G 361
DB 361 G 361

RESULT 2
US-08-838-151A-6
Sequence 6, Application US/08838151A
Publication No. US20010011379A1
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
ADDRESSES: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978

REFERENCE/DOCKET NUMBER: SVS3801B0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-6

Query Match 98.1%; Score 1902; DB 8; Length 361;
Best Local Similarity 98.1%; Pred. No. 3,8e-162;
Matches 354; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPPPKFRVOSKNYFLTYPOCSLSKEBALSQLONTLPVKKFKIKICREIHENGEPHLAV 60
DB 1 MPPPKFRVOSKNYFLTYPOCSLSKEBALSQLONTLPVKKFKIKICREIHENGEPHLAV 60
QY 61 LVQPEGKYQCTNNRFPDLVSPTRSAHPHPIQAKSSSDVKSVIDKDGDTIEWGDFQIDG 120
DB 61 LVQPEGKYQCTNNRFPDLVSPTRSAHPHPIQAKSSSDVKSVIDKDGDTIEWGDFQIDG 120
QY 121 RSARGGQGSANDSYAKALNAGSVOSALAVLREOPKDFVLQNNHRSNLERIFAKAPEPW 180
DB 121 RSARGGQGSANDSYAKALNAGSVOSALAVLREOPKDFVLQNNHRSNLERIFAKAPEPW 180
QY 181 VPPFOVSSFTNVDEMOMADNYFGTGDAAPDRPVSIIEGDSRTGKTMAALGPHNY 240
DB 181 VPPFOVSSFTNVDEMOMADNYFGTGDAAPDRPVSIIEGDSRTGKTMAALGPHNY 240
QY 241 LSGHLDNFGVPSNDVOYNYIDIAPIHYLKLKMKELGAKOMQSNCKYKGPVQIKGI 300
DB 241 LSGHLDNFGVPSNDVOYNYIDIAPIHYLKLKMKELGAKOMQSNCKYKGPVQIKGI 300
QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQSTQASQETGNQAK 360
DB 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQSTQASQETGNQAK 360
QY 361 G 361
DB 361 G 361

RESULT 3
US-08-838-151A-8
Sequence 8, Application US/08838151A
Publication No. US20010011379A1
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
ADDRESSES: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:

```

; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
; US-08-838-151A-8

Query Match          97.6%; Score 1892; DB 8; Length 361;
Best Local Similarity 97.8%; Pred. No. 3e-161;
Matches 353; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MPPKKFRVQSKNYFLTYPCSLSKKEALSQLONLTPVKKFKIKRELHENGEPHLHY 60
DB 1 MPPKKFRVQSKNYFLTYPCSLSKKEALSQLONLTPVKKFKIKRELHENGEPHLHY 60
QY 61 LVQFEKRYQCTNNRFPDLVSPTRSAHFHFNIOGAKSSDVKSITDDGDTIEWGDFQIDG 120
DB 61 LVQFEKRYQCTNNRFPDLVSPTRSAHFHFNIOGAKSSDVKSITDDGDTIEWGDFQIDG 120
QY 121 RSARGGQSQSANDSYAKALNAGSVQSLAVLREBPDPFVLQNNHINSNLERIPAKAPEPW 180
DB 121 RSARGGQSQSANDSYAKALNAGSVQSLAVLREBPDPFVLQNNHINSNLERIPAKAPEPW 180
QY 181 VPPFQVSSFTNVDEQEWADNYFGTGAAPRPPVSIIVEGDSRTGKTMMARALGPBNY 240
DB 181 VPPFQVSSFTNVDEQEWADNYFGTGAAPRPPVSIIVEGDSRTGKTMMARALGPBNY 240
QY 241 LSGHLDPNRVRVNDVQYVNIIDIAPIHYLKLKMKKELLAGQKDWQSNCKYKGVQIKGGI 300
DB 241 LSGHLDPNRVRVNDVQYVNIIDIAPIHYLKLKMKKELLAGQKDWQSNCKYKGVQIKGGI 300
QY 301 PAIVLCNPGEGASYKEFLDKAENTGKKNWTIKNAIFITLTAPLYQSTQASQETGNQKQ 360
DB 301 PAIVLCNPGEGASYKEFLDKAENTGKKNWTIKNAIFITLTAPLYQSTQASQETGNQKQ 360
QY 361 G 361
DB 361 G 361

RESULT 4
US-08-838-151A-4
; Sequence 4, Application US/08838151A
; Publication No. US20010011379A1
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
; US-08-838-151A-4

Query Match          97.3%; Score 1886; DB 8; Length 361;
Best Local Similarity 97.5%; Pred. No. 1e-160;
Matches 352; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 MPPKKFRVQSKNYFLTYPCSLSKKEALSQLONLTPVKKFKIKRELHENGEPHLHY 60
DB 1 MPPKKFRVQSKNYFLTYPCSLSKKEALSQLONLTPVKKFKIKRELHENGEPHLHY 60
QY 61 LVQFEKRYQCTNNRFPDLVSPTRSAHFHFNIOGAKSSDVKSITDDGDTIEWGDFQIDG 120
DB 61 LVQFEKRYQCTNNRFPDLVSPTRSAHFHFNIOGAKSSDVKSITDDGDTIEWGDFQIDG 120
QY 121 RSARGGQSQSANDSYAKALNAGSVQSLAVLREBPDPFVLQNNHINSNLERIPAKAPEPW 180
DB 121 RSARGGQSQSANDSYAKALNAGSVQSLAVLREBPDPFVLQNNHINSNLERIPAKAPEPW 180
QY 181 VPPFQVSSFTNVDEQEWADNYFGTGAAPRPPVSIIVEGDSRTGKTMMARALGPBNY 240
DB 181 VPPFQVSSFTNVDEQEWADNYFGTGAAPRPPVSIIVEGDSRTGKTMMARALGPBNY 240
QY 241 LSGHLDPNRVRVNDVQYVNIIDIAPIHYLKLKMKKELLAGQKDWQSNCKYKGVQIKGGI 300
DB 241 LSGHLDPNRVRVNDVQYVNIIDIAPIHYLKLKMKKELLAGQKDWQSNCKYKGVQIKGGI 300
QY 301 PAIVLCNPGEGASYKEFLDKAENTGKKNWTIKNAIFITLTAPLYQSTQASQETGNQKQ 360
DB 301 PAIVLCNPGEGASYKEFLDKAENTGKKNWTIKNAIFITLTAPLYQSTQASQETGNQKQ 360
QY 361 G 361
DB 361 G 361

RESULT 5
US-08-838-151A-44
; Sequence 44, Application US/08838151A
; Publication No. US20010011379A1
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-44
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```
Query Match      81.1%; Score 1572; DB 8; Length 353;
Best Local Similarity 80.4%; Pred. No. 1,7e-132;
Matches 283; Conservative 31; Mismatches 38; Indels 0; Gaps 0;
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QY 1 MPPPKFRVQSKNYFLTYPOCSLSKEBALSQLONLNTPVNKKIKICREIHENGEPHLAV 60
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Db 1 MPPPKFRVQSKNYFLTYPRCPPIKPEBVLSQLKHATNKKIKVCEBHEHNGEPHLAA 60
QY 61 LVQFEGVQCTNNRFPDLVPTSAHFHPNIOGAKSSDVKSYIDKQDGTIEMGDFQIDG 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LIOFEGFVCTNKRFLDLVSTSAHFHPNIOGAKSSDVKAYIDKQGVITIEGQFQVDG 120
QY 121 RSARGGQGSANDSYAKALNAGVOSALAVIREOPKDFVLQNNHNSLNERIFAKAEPW 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 RSARGGQGSANDSYAKALNADSIESTALTILKEQPKDYVLQNNHNSLNERIFAKVEPW 180
QY 181 VPPPOVSSFTNVVDENQEMADNTFGTGDAAAPRRPVSIIVEGDSRTGKTMAARALGPHNY 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 VPPPLSSFTNVVQEWVDYDFGRGSARPERPISIIIEGDSRTGKTMAARALGPHNY 240
QY 241 LSGHLDPNGVFNVDYQYNYIDIDAPHYLKLKMKKELIGAOKMOSCKYKGPVQIKGI 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 LSGHLDPNSRVSNVAEYNYIDIDISPNYKLKMKKELIGAOKMOSCKYKGPVQIKGI 300
QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYOESTQASQ 352
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 PSIVLCNPGEGSSYKDFLDKENRALHNTIHNALFVTLTAPLYQSTTQDCQ 352
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RESULT 6
US-08-838-151A-46
; Sequence 46, Application US/08838151A
; Publication No. US20010011379A1
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing GeminiViruses
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-46
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Query Match      81.1%; Score 1572; DB 8; Length 353;
Best Local Similarity 80.4%; Pred. No. 1,7e-132;
Matches 283; Conservative 31; Mismatches 38; Indels 0; Gaps 0;
```

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QY 1 MPPPKFRVQSKNYFLTYPOCSLSKEBALSQLONLNTPVNKKIKICREIHENGEPHLAV 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MPPPKFRVQSKNYFLTYPRCPPIKPEBVLSQLKHATNKKIKVCEBHEHNGEPHLAA 60
QY 61 LVQFEGVQCTNNRFPDLVPTSAHFHPNIOGAKSSDVKSYIDKQDGTIEMGDFQIDG 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LIOFEGFVCTNKRFLDLVSTSAHFHPNIOGAKSSDVKAYIDKQGVITIEGQFQVDG 120
QY 121 RSARGGQGSANDSYAKALNAGVOSALAVIREOPKDFVLQNNHNSLNERIFAKAEPW 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 RSARGGQGSANDSYAKALNADSIESTALTILKEQPKDYVLQNNHNSLNERIFAKVEPW 180
QY 181 VPPPOVSSFTNVVDENQEMADNTFGTGDAAAPRRPVSIIVEGDSRTGKTMAARALGPHNY 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 VPPPLSSFTNVVQEWVDYDFGRGSARPERPISIIIEGDSRTGKTMAARALGPHNY 240
QY 241 LSGHLDPNGVFNVDYQYNYIDIDAPHYLKLKMKKELIGAOKMOSCKYKGPVQIKGI 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 LSGHLDPNSRVSNVAEYNYIDIDISPNYKLKMKKELIGAOKMOSCKYKGPVQIKGI 300
QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYOESTQASQ 352
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 PSIVLCNPGEGSSYKDFLDKENRALHNTIHNALFVTLTAPLYQSTTQDCQ 352
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RESULT 7
US-08-838-151A-49
; Sequence 49, Application US/08838151A
; Publication No. US20010011379A1
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing GeminiViruses
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-49
```

```
Query Match      80.8%; Score 1567; DB 8; Length 353;
Best Local Similarity 80.1%; Pred. No. 4.8e-132;
Matches 282; Conservative 31; Mismatches 39; Indels 0; Gaps 0;
```

```
QY 1 MPPPKFRVQSKNYFLTYPCQSLKKEALSQLQNLNTPVNNKFKIKICRELHENGEPHLAV 60
DB 1 MPPPKFRVQSKNYFLTYPCQSLKKEALSQLQNLNTPVNNKFKIKICRELHENGEPHLAV 60
QY 61 LVQFEGKYQCTNNRFPDLVSPTRSAHFHNPINQAKSSSDVKSYYIDKQDTIEWGDFQIDG 120
DB 61 LVQFEGKYQCTNNRFPDLVSPTRSAHFHNPINQAKSSSDVKSYYIDKQDTIEWGDFQIDG 120
QY 121 RSARGGQOSANDSYAALNAGSVOALAVREBPDPFVLQNNHNSNLERIFAKAPEPW 180
DB 121 RSARGGQOSANDSYAALNAGSVOALAVREBPDPFVLQNNHNSNLERIFAKAPEPW 180
QY 181 VPPFOVSSFTNVDEQEWADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
DB 181 VPPFOVSSFTNVDEQEWADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
QY 241 LSGHLDENGRVPSNDVQYNNVIDIAPHYLKLKHWKELGAQKDWQSNCKYKGPVQIKGGI 300
DB 241 LSGHLDENGRVPSNDVQYNNVIDIAPHYLKLKHWKELGAQKDWQSNCKYKGPVQIKGGI 300
QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNTIKNAIFITLTAPLYQSTQASQ 352
DB 301 PAIVLCNPGEGASYKEFLDKAENTGLKNTIKNAIFITLTAPLYQSTQASQ 352
QY 301 PSIVLCNPGEGSSYKDFLDKEENRALHNMTHNAIFVTLTAPLYQSTQDCQ 352
DB 301 PSIVLCNPGEGSSYKDFLDKEENRALHNMTHNAIFVTLTAPLYQSTQDCQ 352
```

RESULT 8
US-08-838-151A-52

```
; Sequence 52, Application US/08838151A
; Publication No. US20010011379A1
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-52
```

```
Query Match      80.8%; Score 1566; DB 8; Length 353;
Best Local Similarity 80.1%; Pred. No. 5.8e-132;
Matches 282; Conservative 31; Mismatches 39; Indels 0; Gaps 0;
```

```
QY 1 MPPPKFRVQSKNYFLTYPCQSLKKEALSQLQNLNTPVNNKFKIKICRELHENGEPHLAV 60
DB 1 MPPPKFRVQSKNYFLTYPCQSLKKEALSQLQNLNTPVNNKFKIKICRELHENGEPHLAV 60
QY 61 LVQFEGKYQCTNNRFPDLVSPTRSAHFHNPINQAKSSSDVKSYYIDKQDTIEWGDFQIDG 120
DB 61 LVQFEGKYQCTNNRFPDLVSPTRSAHFHNPINQAKSSSDVKSYYIDKQDTIEWGDFQIDG 120
QY 121 RSARGGQOSANDSYAALNAGSVOALAVREBPDPFVLQNNHNSNLERIFAKAPEPW 180
DB 121 RSARGGQOSANDSYAALNAGSVOALAVREBPDPFVLQNNHNSNLERIFAKAPEPW 180
QY 181 VPPFOVSSFTNVDEQEWADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
DB 181 VPPFOVSSFTNVDEQEWADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
QY 241 LSGHLDENGRVPSNDVQYNNVIDIAPHYLKLKHWKELGAQKDWQSNCKYKGPVQIKGGI 300
DB 241 LSGHLDENGRVPSNDVQYNNVIDIAPHYLKLKHWKELGAQKDWQSNCKYKGPVQIKGGI 300
QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNTIKNAIFITLTAPLYQSTQASQ 352
DB 301 PAIVLCNPGEGASYKEFLDKAENTGLKNTIKNAIFITLTAPLYQSTQASQ 352
QY 301 PSIVLCNPGEGSSYKDFLDKEENRALHNMTHNAIFVTLTAPLYQSTQDCQ 352
DB 301 PSIVLCNPGEGSSYKDFLDKEENRALHNMTHNAIFVTLTAPLYQSTQDCQ 352
```

RESULT 9
US-08-838-151A-55

```
; Sequence 55, Application US/08838151A
; Publication No. US20010011379A1
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-55

```

```

Query Match      80.7%; Score 1564; DB 8; Length 353;
Best Local Similarity 80.1%; Pred. No. 8.8e-132;
Matches 282; Conservative 31; Mismatches 39; Indels 0; Gaps 0;

```

```

QY 1 MPPPKRRVQSKNYFLTYPCSLSKKEALSQLQNLNTPVKKFKIKRELHNGEPHLAV 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MPPPKRRVQSKNYFLTYPCSLSKKEALSQLQNLNTPVKKFKIKRELHNGEPHLA 60

QY 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFPHNIQAKSSDVKSYIDKGDPTIEMGDFQID 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFPHNIQAKSSDVKAYIDKGVITIEGQFOVD 120

QY 121 RSARGGQGSANDSYAKALNAGVQSALAVLREOPKDFVLQNHNRISNLERIPAKAPEPW 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 RSARGGQGSANDSYAKALNAGVQSALAVLREOPKDFVLQNHNRISNLERIPAKAPEPW 180

QY 121 RSARGGQGSANDSYAKALNAGVQSALAVLREOPKDFVLQNHNRISNLERIPAKAPEPW 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 RSARGGQGSANDSYAKALNAGVQSALAVLREOPKDFVLQNHNRISNLERIPAKAPEPW 180

QY 181 VPPFQVSSFTNVPDEMOMADNYFTGDDAAPDRPVSIIVEGDSRTGKTMAALGPHNY 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 VPPFQVSSFTNVPDEMOMADNYFTGDDAAPDRPVSIIVEGDSRTGKTMAALGPHNY 240

QY 181 VPPFQVSSFTNVPDEMOMADNYFTGDDAAPDRPVSIIVEGDSRTGKTMAALGPHNY 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 VPPFQVSSFTNVPDEMOMADNYFTGDDAAPDRPVSIIVEGDSRTGKTMAALGPHNY 240

QY 241 LSGHLDENGVRFSNDVQYVVIDIAAPHYLKLGKMKELIGAQRDMQWNCCKYKGPVQIKG 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 LSGHLDENGVRFSNDVQYVVIDIAAPHYLKLGKMKELIGAQRDMQWNCCKYKGPVQIKG 300

QY 241 LSGHLDENGVRFSNDVQYVVIDIAAPHYLKLGKMKELIGAQRDMQWNCCKYKGPVQIKG 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 LSGHLDENGVRFSNDVQYVVIDIAAPHYLKLGKMKELIGAQRDMQWNCCKYKGPVQIKG 300

QY 301 PAIVLCNPEGASYSKEFLDKAENTGLKNWTIKNAIFITLTAPLYOESTOASQ 352
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 PAIVLCNPEGASYSKEFLDKAENTGLKNWTIKNAIFITLTAPLYOESTOASQ 352

QY 301 PAIVLCNPEGASYSKEFLDKAENTGLKNWTIKNAIFITLTAPLYOESTOASQ 352
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 PAIVLCNPEGASYSKEFLDKAENTGLKNWTIKNAIFITLTAPLYOESTOASQ 352

```

```

RESULT 10
US-10-633-850-80
; Sequence 80, Application US/10633850
; Publication No. US20040205843A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.4581P
; CURRENT APPLICATION NUMBER: US/10/633, 850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 80
; LENGTH: 352

```

```

; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; US-10-633-850-80

```

```

Query Match      77.6%; Score 1504.5; DB 17; Length 352;
Best Local Similarity 75.9%; Pred. No. 2e-126;
Matches 267; Conservative 44; Mismatches 40; Indels 1; Gaps 1;

```

```

QY 1 MPPPKRRVQSKNYFLTYPCSLSKKEALSQLQNLNTPVKKFKIKRELHNGEPHL 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MPPPKRRVQSKNYFLTYPCSLSKKEALSQLQNLNTPVKKFKIKRELHNGEPHL 60

QY 60 LVQPEGKYQCTNNRFPDLVSPTRSAHFPHNIQAKSSDVKSYIDKGDPTIEMGDFQID 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 60 LVQPEGKYQCTNNRFPDLVSPTRSAHFPHNIQAKSSDVKSYIDKGDPTIEMGDFQID 120

QY 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFPHNIQAKSSDVKSYIDKGDPTIEMGDFQID 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFPHNIQAKSSDVKSYIDKGDPTIEMGDFQID 120

QY 120 GRSARGGQGSANDSYAKALNAGVQSALAVLREOPKDFVLQNHNRISNLERIPAKAPEP 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 120 GRSARGGQGSANDSYAKALNAGVQSALAVLREOPKDFVLQNHNRISNLERIPAKAPEP 180

QY 121 GRSARGGQGSANDSYAKALNAGVQSALAVLREOPKDFVLQNHNRISNLERIPAKAPEP 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 GRSARGGQGSANDSYAKALNAGVQSALAVLREOPKDFVLQNHNRISNLERIPAKAPEP 180

QY 180 VPPFQVSSFTNVPDEMOMADNYFTGDDAAPDRPVSIIVEGDSRTGKTMAALGPHN 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 180 VPPFQVSSFTNVPDEMOMADNYFTGDDAAPDRPVSIIVEGDSRTGKTMAALGPHN 240

QY 181 VPPFQVSSFTNVPDEMOMADNYFTGDDAAPDRPVSIIVEGDSRTGKTMAALGPHN 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 VPPFQVSSFTNVPDEMOMADNYFTGDDAAPDRPVSIIVEGDSRTGKTMAALGPHN 240

QY 240 YLSGHLDENGVRFSNDVQYVVIDIAAPHYLKLGKMKELIGAQRDMQWNCCKYKGPVQIKG 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 240 YLSGHLDENGVRFSNDVQYVVIDIAAPHYLKLGKMKELIGAQRDMQWNCCKYKGPVQIKG 239

QY 241 YLSGHLDENGVRFSNDVQYVVIDIAAPHYLKLGKMKELIGAQRDMQWNCCKYKGPVQIKG 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 YLSGHLDENGVRFSNDVQYVVIDIAAPHYLKLGKMKELIGAQRDMQWNCCKYKGPVQIKG 300

QY 300 IPAILVLCNPEGASYSKEFLDKAENTGLKNWTIKNAIFITLTAPLYOESTOAS 351
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 300 IPAILVLCNPEGASYSKEFLDKAENTGLKNWTIKNAIFITLTAPLYOESTOAS 352

QY 301 IPAILVLCNPEGASYSKEFLDKAENTGLKNWTIKNAIFITLTAPLYOESTOAS 352
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 IPAILVLCNPEGASYSKEFLDKAENTGLKNWTIKNAIFITLTAPLYOESTOAS 352

```

```

RESULT 11
US-10-633-850-84
; Sequence 84, Application US/10633850
; Publication No. US20040205843A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Gruijssem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.4581P
; CURRENT APPLICATION NUMBER: US/10/633,850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 84
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; US-10-633-850-84

```

```

Query Match      77.5%; Score 1503.5; DB 17; Length 352;
Best Local Similarity 75.9%; Pred. No. 2.4e-126;
Matches 267; Conservative 45; Mismatches 39; Indels 1; Gaps 1;

```

```

QY 1 MPPPKRRVQSKNYFLTYPCSLSKKEALSQLQNLNTPVKKFKIKRELHNGEPHL 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MPPPKRRVQSKNYFLTYPCSLSKKEALSQLQNLNTPVKKFKIKRELHNGEPHL 60

QY 60 LVQPEGKYQCTNNRFPDLVSPTRSAHFPHNIQAKSSDVKSYIDKGDPTIEMGDFQID 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 60 LVQPEGKYQCTNNRFPDLVSPTRSAHFPHNIQAKSSDVKSYIDKGDPTIEMGDFQID 120

QY 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFPHNIQAKSSDVKSYIDKGDPTIEMGDFQID 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFPHNIQAKSSDVKSYIDKGDPTIEMGDFQID 120

QY 120 GRSARGGQGSANDSYAKALNAGVQSALAVLREOPKDFVLQNHNRISNLERIPAKAPEP 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 120 GRSARGGQGSANDSYAKALNAGVQSALAVLREOPKDFVLQNHNRISNLERIPAKAPEP 180

QY 121 GRSARGGQGSANDSYAKALNAGVQSALAVLREOPKDFVLQNHNRISNLERIPAKAPEP 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 GRSARGGQGSANDSYAKALNAGVQSALAVLREOPKDFVLQNHNRISNLERIPAKAPEP 180

```



```

QY      180 WVPFVQSSFTNTPDEMOEWADNYFTGNDAAAPDRPVSIIVEGDSRTGKTMARALGPHN 239
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 WVPFVSSFTNTPDEMOEWADNYFTGNDAAAPDRPVSIIVEGDSRTGKTMARALGPHN 240
QY      240 YLSGHLDFNGRVSNQVYNNVIDDIAPHYLKLGHWKELGAGQDMQSNCKYGRPVQIKGG 239
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 YLSGHLDFNGRVSNQVYNNVIDDIAPHYLKLGHWKELGAGQDMQSNCKYGRPVQIKGG 300
QY      300 IPAIVLCNPEGASYSKFEFLDKAENTGLKMTIKNAIFITLTAPLYOESTQAS 351
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      301 IPSIVLCNPEGASYSKFEFLDKAENTGLKMTIFHNAKVFVFLNSPLYOSTQSS 352

```

RESULT 12
US-10-633-850-1
Sequence 1, Application US/10633850
Publication No. US20040205843A1
GENERAL INFORMATION:
APPLICANT: Hanley-Bowdoin, Linda
APPLICANT: Orozco, Beverly M.
APPLICANT: Gruijssem, Wilhelm
TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
FILE REFERENCE: 5051.4581P
CURRENT APPLICATION NUMBER: US/10/633,850
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 09/289,346
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 60/125,004
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 352
TYPE: PRT
ORGANISM: Tomato golden mosaic virus
US-10-633-850-1

```

Query Match      77.5%; Score 1502.5; DB 17; Length 352;
Best Local Similarity 75.9%; Pred. No. 3e-126;
Matches 267; Conservative 44; Mismatches 40; Indels 1; Gaps 1;
QY      1 MP-PPKFRVQSNKYFLTYPQCSLSKEBALSQLQNTPTVNNKFKIKICREHNGEPHLM 59
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MESHPRRFOINAKNYFLTYPQCSLSKEBSLSQALNTPIKKFKIKICREHNGEPHLM 60
QY      60 VLVQFEGKYQCTNNRPFEDLVSPTRSAHFHFNIGAKSSSDVKSXIDKDGDTIEWGDFQID 119
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 VLVQFEGKYCCQNRFFDLVSPTRSAHFHFNIGAKSSSDVKSXIDKDGDTIEWGDFQID 120
QY      120 GRSARGGQOSANDSYAKALNAGSVQALAVLREBOPDFVLQNHNTRSNLERIFAKAPBP 179
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 GRSARGGQOSNDAAEALNASSKEALQIRREKIPKYLQFPHNLSNLDRIFDKPEP 180
QY      180 WVPFVQSSFTNTPDEMOEWADNYFTGNDAAAPDRPVSIIVEGDSRTGKTMARALGPHN 239
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 WVPFVSSFTNTPDEMOEWADNYFTGNDAAAPDRPVSIIVEGDSRTGKTMARALGPHN 240
QY      240 YLSGHLDFNGRVSNQVYNNVIDDIAPHYLKLGHWKELGAGQDMQSNCKYGRPVQIKGG 239
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 YLSGHLDFNGRVSNQVYNNVIDDIAPHYLKLGHWKELGAGQDMQSNCKYGRPVQIKGG 300
QY      300 IPAIVLCNPEGASYSKFEFLDKAENTGLKMTIKNAIFITLTAPLYOESTQAS 351
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      301 IPSIVLCNPEGASYSKFEFLDKAENTGLKMTIFHNAKVFVFLNSPLYOSTQSS 352

```

RESULT 13
US-10-633-850-64
Sequence 64, Application US/10633850
Publication No. US20040205843A1
GENERAL INFORMATION:
APPLICANT: Hanley-Bowdoin, Linda
APPLICANT: Orozco, Beverly M.

```

APPLICANT: Gruijssem, Wilhelm
TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
FILE REFERENCE: 5051.4581P
CURRENT APPLICATION NUMBER: US/10/633,850
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 09/289,346
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 60/125,004
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn version 3.2
SEQ ID NO 64
LENGTH: 352
TYPE: PRT
ORGANISM: Tomato golden mosaic virus
US-10-633-850-64

```

```

Query Match      77.5%; Score 1502.5; DB 17; Length 352;
Best Local Similarity 75.9%; Pred. No. 3e-126;
Matches 267; Conservative 44; Mismatches 40; Indels 1; Gaps 1;
QY      1 MP-PPKFRVQSNKYFLTYPQCSLSKEBALSQLQNTPTVNNKFKIKICREHNGEPHLM 59
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MESHPRRFOINAKNYFLTYPQCSLSKEBSLSQALNTPIKKFKIKICREHNGEPHLM 60
QY      60 VLVQFEGKYQCTNNRPFEDLVSPTRSAHFHFNIGAKSSSDVKSXIDKDGDTIEWGDFQID 119
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 VLVQFEGKYCCQNRFFDLVSPTRSAHFHFNIGAKSSSDVKSXIDKDGDTIEWGDFQID 120
QY      120 GRSARGGQOSANDSYAKALNAGSVQALAVLREBOPDFVLQNHNTRSNLERIFAKAPBP 179
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 GRSARGGQOSNDAAEALNASSKEALQIRREKIPKYLQFPHNLSNLDRIFDKPEP 180
QY      180 WVPFVQSSFTNTPDEMOEWADNYFTGNDAAAPDRPVSIIVEGDSRTGKTMARALGPHN 239
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 WVPFVSSFTNTPDEMOEWADNYFTGNDAAAPDRPVSIIVEGDSRTGKTMARALGPHN 240
QY      240 YLSGHLDFNGRVSNQVYNNVIDDIAPHYLKLGHWKELGAGQDMQSNCKYGRPVQIKGG 239
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 YLSGHLDFNGRVSNQVYNNVIDDIAPHYLKLGHWKELGAGQDMQSNCKYGRPVQIKGG 300
QY      300 IPAIVLCNPEGASYSKFEFLDKAENTGLKMTIKNAIFITLTAPLYOESTQAS 351
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      301 IPSIVLCNPEGASYSKFEFLDKAENTGLKMTIFHNAKVFVFLNSPLYOSTQSS 352

```

RESULT 14
US-10-633-850-86
Sequence 86, Application US/10633850
Publication No. US20040205843A1
GENERAL INFORMATION:
APPLICANT: Hanley-Bowdoin, Linda
APPLICANT: Orozco, Beverly M.
APPLICANT: Gruijssem, Wilhelm
TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
FILE REFERENCE: 5051.4581P
CURRENT APPLICATION NUMBER: US/10/633,850
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 09/289,346
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 60/125,004
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn version 3.2
SEQ ID NO 86
LENGTH: 352
TYPE: PRT
ORGANISM: Tomato golden mosaic virus
US-10-633-850-86

Query Match 77.4%; Score 1500.5; DB 17; Length 352;
Best Local Similarity 75.9%; Pred. No. 4.5e-126;
Matches 267; Conservative 44; Mismatches 40; Indels 1; Gaps 1;

```
QY 1 MPP-PKKERVQSKNYFLTYPOCSLSKEBALSQLONTLPVKKFKIKICREIHENGEPHL 59
Db 1 MPP-PKKERVQSKNYFLTYPOCSLSKEBALSQLONTLPVKKFKIKICREIHENGEPHL 60
QY 60 VLVQFEGKYQCTNNRFPDLVSPTRSAHFHPIIQAKSSDVKSYIDKDGDTIEWDFOID 119
Db 61 VLVQFEGKYQCTNNRFPDLVSPTRSAHFHPIIQAKSSDVKSYIDKDGDTIEWDFOID 120
QY 120 GRSARGGQOQSNDSYAKALNAGSVQALAVIREQOPDVLQNNHNSNLERIPAKAPER 179
Db 121 GRSARGGQOQSNDSYAKALNAGSVQALAVIREQOPDVLQNNHNSNLERIPAKAPER 180
QY 180 WVPFVOYSSFTNVDEMOMANDYFGTGDAPDPDPVSIIEGDSRTGKTMMARALGPHN 239
Db 181 WVPFVOYSSFTNVDEMOMANDYFGTGDAPDPDPVSIIEGDSRTGKTMMARALGPHN 240
QY 240 YLSGHLDFNGRVFNSNDVQYVNIIDIAPHYLLKHKMKELGAQKQWQSNCKYKGPVQIKG 299
Db 241 YLSGHLDFNGRVFNSNDVQYVNIIDIAPHYLLKHKMKELGAQKQWQSNCKYKGPVQIKG 300
QY 300 IPAIVLCNPGEGASYKEFLDKAENTGLKNWTKNAIFITLTAPLYQESTQAS 351
Db 301 IPAIVLCNPGEGASYKEFLDKAENTGLKNWTKNAIFITLTAPLYQESTQAS 352
```

RESULT 15

```
US-10-613-850-82
; Sequence 82, Application US/10631850
; Publication No. US20040205843A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Griseem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.4581P
; CURRENT APPLICATION NUMBER: US/10/633, 850
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-10-613-850-82
```

Query Match 77.3%; Score 1499.5; DB 17; Length 352;

Best Local Similarity 75.9%; Pred. No. 5.5e-126; Matches 267; Conservative 43; Mismatches 41; Indels 1; Gaps 1;

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QY 1 MPP-PKKERVQSKNYFLTYPOCSLSKEBALSQLONTLPVKKFKIKICREIHENGEPHL 59
Db 1 MPP-PKKERVQSKNYFLTYPOCSLSKEBALSQLONTLPVKKFKIKICREIHENGEPHL 60
QY 60 VLVQFEGKYQCTNNRFPDLVSPTRSAHFHPIIQAKSSDVKSYIDKDGDTIEWDFOID 119
Db 61 VLVQFEGKYQCTNNRFPDLVSPTRSAHFHPIIQAKSSDVKSYIDKDGDTIEWDFOID 120
QY 120 GRSARGGQOQSNDSYAKALNAGSVQALAVIREQOPDVLQNNHNSNLERIPAKAPER 179
Db 121 GRSARGGQOQSNDSYAKALNAGSVQALAVIREQOPDVLQNNHNSNLERIPAKAPER 180
QY 180 WVPFVOYSSFTNVDEMOMANDYFGTGDAPDPDPVSIIEGDSRTGKTMMARALGPHN 239
Db 181 WVPFVOYSSFTNVDEMOMANDYFGTGDAPDPDPVSIIEGDSRTGKTMMARALGPHN 240
QY 240 YLSGHLDFNGRVFNSNDVQYVNIIDIAPHYLLKHKMKELGAQKQWQSNCKYKGPVQIKG 299
Db 241 YLSGHLDFNGRVFNSNDVQYVNIIDIAPHYLLKHKMKELGAQKQWQSNCKYKGPVQIKG 300
```

```
QY 300 IPAIVLCNPGEGASYKEFLDKAENTGLKNWTKNAIFITLTAPLYQESTQAS 351
Db 301 IPAIVLCNPGEGASYKEFLDKAENTGLKNWTKNAIFITLTAPLYQESTQAS 352
```

Search completed: December 3, 2004, 15:13:08
Job time: 145 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2004, 14:57:49 ; Search time 48 Seconds
(without alignments)
723.630 Million cell updates/sec

Title: US-09-491-063A-2

Sequence: 1 MEPPKKFRVQSKNYFLTYPO.....PLYQSTQASQETGNQAKG 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1920	99.0	358	1 JQ1870	Al1 protein - toma
2	1572	81.1	361	1 QOCVPT	Al1 protein - pota
3	1562	80.6	355	1 QOCVW1	Al1 protein - abut
4	1502.5	77.5	352	1 QOCVLI	Al1 protein - toma
5	1344	69.3	385	2 S28360	Al1 protein - beet
6	1340.5	69.1	362	1 JQ1887	Al1 protein - toma
7	1338.5	69.0	349	2 JQ2300	replicase - pepper
8	1338.5	69.0	349	2 S31875	Al1 protein - pepp
9	1311.5	67.6	359	2 S22593	hypotheical prote
10	1310.5	67.6	360	2 S59885	replication-associ
11	1307	67.4	351	2 JQ2327	Al1 protein - indi
12	1305.5	67.3	359	2 S39211	gene C1 protein -
13	1296.5	66.9	357	1 QOCVCI	Al1 protein - toma
14	1290.5	66.1	359	2 S39235	gene C1 protein -
15	1282.5	66.6	358	2 S07594	hypotheical prote
16	1166.5	60.2	347	1 QOCVSI	Al1 protein - equa
17	464.5	24.0	351	2 S49387	replication-associ
18	461.5	23.8	351	2 B24356	replication-associ
19	409.5	21.1	411	2 S45059	Al1 protein (clone
20	268	13.8	411	1 QOCVPZ	p1 polypeptide - m
21	254.5	13.1	217	2 JQ1358	C1 protein - misca
22	250	12.9	146	2 C42452	C1 protein - tobac
23	248	12.8	295	2 D42452	C1 protein - tobac
24	246	12.7	295	2 JU0043	hypotheical 33.2K
25	238	12.3	136	2 JQ1359	C2 protein - misca
26	202.5	10.4	272	2 A05158	hypotheical prote
27	199.5	10.3	272	2 JQ1553	C2 protein - panic
28	199.5	10.3	272	2 S04806	hypotheical prote
29	196.5	10.1	272	2 T10116	replication protei

30	191.5	9.9	153	2 T10115	replication-associ
31	188.5	9.7	148	2 S04807	hypotheical prote
32	187.5	9.7	136	2 JU0044	hypotheical 15.8K
33	177	9.1	333	2 JQ1552	C1 protein - panic
34	161.5	8.3	84	2 PS0142	replication-associ
35	105	5.4	979	2 T50956	hypotheical prote
36	102.5	5.3	562	1 UKHUT	t-plasminogen acti
37	102.5	5.3	1244	2 S73731	probable lipoprote
38	98.5	5.1	2116	2 A26655	myosin heavy chain
39	97	5.0	356	2 E81269	hypotheical prote
40	96.5	5.0	287	1 PMVKL	inorganic diphosph
41	96	5.0	421	2 AG2587	lytic murein trans
42	96	5.0	421	2 G97369	hypotheical prote
43	96	5.0	539	2 D83764	chitinase B90916
44	96	5.0	1203	1 A47501	nitric-oxide synth
45	95	4.9	472	2 F86702	hypotheical prote

ALIGNMENTS

```
RESULT 1
JQ1870
Al1 protein - tomato mottle virus (isolate Florida)
C/Species: tomato mottle virus
C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
R/Accession: JQ1870
R/Abouzeid, A.M.; Polston, J.E.; Hiebert, E.
J. Gen. Virol. 73, 3225-3229, 1992
A/Title: The nucleotide sequence of tomato mottle virus, a new geminivirus isolated from
A/Reference number: JQ1869; NCBI:3107858; PMID:1469361
A/Accession: JQ1870
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-358 <ABO>
A/Cross-references: UNIPROT:Q06657; GB:L14460
C/Genetics:
A/Map position: segment A
C/Superfamily: tomato golden mosaic virus Al1 protein

Query Match          99.0%; Score 1920; DB 1; Length 358;
Best Local Similarity 100.0%; Pred. No. 8, 1e-141;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKKFRVQSKNYFLTYPOCSLSKEALSQQLNTLPVKKFKIKRELHENGEPHLVLYQ 63
DB 1 PKKFRVQSKNYFLTYPOCSLSKEALSQQLNTLPVKKFKIKRELHENGEPHLVLYQ 60

QY 64 FEGRYQCTNNRFPDLVSPTRSAHFPHNIQAKSSDVKSYYIDQDGTIEWGDIQIDGRSA 123
DB 61 FEGRYQCTNNRFPDLVSPTRSAHFPHNIQAKSSDVKSYYIDQDGTIEWGDIQIDGRSA 120

QY 124 RGGQOSANDSYAKALNAGSYQSLAVLREBPQDPFLQNNINIRSNLERIPAKAPEPVVP 183
DB 121 RGGQOSANDSYAKALNAGSYQSLAVLREBPQDPFLQNNINIRSNLERIPAKAPEPVVP 180

QY 184 FOVSFTNVDENQEWADNYFGTDAAPDPDPVSIIVEGDSRTQKTMMARALCPHNYLSG 243
DB 181 FOVSFTNVDENQEWADNYFGTDAAPDPDPVSIIVEGDSRTQKTMMARALCPHNYLSG 240

QY 244 HLPNGRVRSNDVQYVNIIDIAHYIKLKKMKELLAGQKDWQSNCKYKGVQIKGIPAI 303
DB 241 HLPNGRVRSNDVQYVNIIDIAHYIKLKKMKELLAGQKDWQSNCKYKGVQIKGIPAI 300

QY 304 VLGPNPBGASYSKEFLDKAENTGKKNWTIKNAIFITTLAPLYQSTQASQETGNQAKG 361
DB 301 VLGPNPBGASYSKEFLDKAENTGKKNWTIKNAIFITTLAPLYQSTQASQETGNQAKG 358

RESULT 2
QOCVPT
Al1 protein - potato yellow mosaic virus (isolate Venezuela)
C/Species: potato yellow mosaic virus
```

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: J00364
R:Conts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.
J. Gen. Virol. 72, 1515-1520, 1991
A>Title: The nucleotide sequence of the infectious cloned DNA components of potato yellow
A:Reference number: J00362; MUID:91311403; PMID:1856690
A:Accession: J00364
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-361 <COU>
C:Cross-references: UNIPROT:P27258; GB:D00940; NID:9222458; PIDN:BAA00782.1; PID:92224555
C:Map position: segment A
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 81.1%; Score 1572; DB 1; length 361;
Best Local Similarity 77.9%; Pred. No. 6.5e-114;
Matches 279; Conservative 39; Mismatches 40; Indels 0; Gaps 0;

1 MPPPKKFFVQSKNFVLTYPQCSLSKEALSDLOLNTFVNNKKFKIKREIHENGEPHLHV 60
1 MPRKGSFIRKAKNFVLTYPQCSLSKEALSDLOLNTFVNNKKFKIKREIHENGEPHLHV 60
1 LIOEGGKYNCTNNRFLDIVSPTRSAHFHPNIOGAKSSSDVKSYYDKDGTTEWGFPOIDG 120
1 LIOEGGKYNCTNNRFLDIVSPTRSAHFHPNIOGAKSSSDVKSYYDKDGTTEWGFPOIDG 120
1 RSAGGCGOOSANDSYAKALNAGSVOSALAVLHEEOPKDFVLONNHRISNLEIFPAKAPBPW 180
1 RSAGGCGOOSANDSYAKALNAGSVOSALAVLHEEOPKDFVLONNHRISNLEIFPAKAPBPW 180
1 VPPFVSSFTNVPPDEMOMADNYPFGTGDAPDPDPVSIIIVEGDSRTCKTMMARALGPHNY 240
1 APPPLSSFTNVPPDEMOMADNYPFGTGDAPDPDPVSIIIVEGDSRTCKTMMARALGPHNY 240
1 LSGLHDFNFRFSDVQVNVVDIAAPHYLLKHKWELLGAKQMSNCKYKGPVOIGGI 300
1 LSGLHDFNFRFSDVQVNVVDIAAPHYLLKHKWELLGAKQMSNCKYKGPVOIGGI 300
1 PSIVLCNGBESSYKAFIDKDEMSLKNWTLKKNVFIITTPVLVEGTQASKEBNGE 358
1 PSIVLCNGBESSYKAFIDKDEMSLKNWTLKKNVFIITTPVLVEGTQASKEBNGE 358

RESULT 3
COCVW1
AV1 protein - abutilon mosaic virus (isolate West India)
C:Species: abutilon mosaic virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: A36214
R:Frishchmidt, T.; Zimmat, G.; Jeske, H.
Virol. 178, 461-468, 1990
A>Title: The nucleotide sequence of the abutilon mosaic virus reveals prokaryotic as well
A:Reference number: A36214; MUID:91020984; PMID:2219703
A:Accession: A36214
A:Molecule type: DNA
A:Residues: 1-355 <FRI>
C:Cross-references: UNIPROT:P21947; EMBL:X15983
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 80.6%; Score 1562; DB 1; length 355;
Best Local Similarity 81.4%; Pred. No. 3.8e-113;
Matches 293; Conservative 22; Mismatches 35; Indels 10; Gaps 3;

1 MPPPKKFFVQSKNFVLTYPQCSLSKEALSDLOLNTFVNNKKFKIKREIHENGEPHLHV 60
1 MPPPKKFFVQSKNFVLTYPQCSLSKEALSDLOLNTFVNNKKFKIKREIHENGEPHLHV 60
1 LVQFEGKYNCTNNRFLDIVSPTRSAHFHPNIOGAKSSSDVKSYYDKDGTTEWGFPOIDG 120
1 LVQFEGKYNCTNNRFLDIVSPTRSAHFHPNIOGAKSSSDVKSYYDKDGTTEWGFPOIDG 120
1 LIOEGGKYNCTNNRFLDIVSPTRSAHFHPNIOGAKSSSDVKSYYDKDGTTEWGFPOIDG 120
1 LIOEGGKYNCTNNRFLDIVSPTRSAHFHPNIOGAKSSSDVKSYYDKDGTTEWGFPOIDG 120

```

QY 121 RSARGCOOSANDSVAKALNAGSVQSLALVREBOPDFLQONNINISNLERIPAKPEPW 180
Db 121 RSARGCOQTANDSVAKALNAGVQSLNLTKEBQPDVYLQONNINISNLERIPAKPEPW 180
QY 181 VPPFQVSSFTVNPDEMOEWADNVPFGTDAAP--PDRPVSIIYEGDSRTGKTMMARALGPH 238
Db 181 VAGFPSPILSRPPRRRCRSGRMIIIG---VPLRPDRPLSLIYEGDSRTGKTMMARALGPH 237
QY 239 NYLSGHLDPNGRVFSSNDVOYNVIDIAPHYLKLKHWKELLGAQKQWQSNCKYKGPVQIKG 298
Db 238 NYLSGHLDPNGRVFSSNEVEYNVIDIAPHYLKLKHWKELLGAQKQWQSNCKLAKPVQIKG 297
QY 299 GIPPAVLVLCNPGGASVYKFLDKAENTGLKNWTTIKNAIFITLTAPLYQESTQASOETGNOK 358
Db 298 GIPPAVLVLCNPGGASVYKFLDKAENTGLKNWTTIKNAIFITLTAPLYQ----GRHTRPR 352

RESULT 4
OOCVLI
A:1 protein - tomato golden mosaic virus
C:Species: tomato golden mosaic virus
A:Note: host Nicotiana sp. (tobacco)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004
C:Accession: A04170
R:Hamilton, W.D.O.; Stein, V.E.; Coutter, R.H.A.; Buck, K.W.
EMBO J. 3, 2197-2205, 1984
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of tomato golden mosaic virus
A:Reference number: A04163
A:Accession: A04170
A:Molecule type: DNA
A:Residues: 1-352 <HAM>
C:Cross-references: UNIPROT:P03567
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A and DNA B.

C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus A11 protein

Query Match 77.5%; Score 1502.5; DB 1; Length 352;
Best Local Similarity 75.9%; Pred. No. 1.5e-108; Mismatches 44; Indels 1; Gaps 1;
Matches 267; Conservative 44;

QY 1 MPP-PPKFPVQSKNFILTYPOCSLSKEBALSQLONTNPVKKFKIKICRELAHNGEBPLH 59
Db 1 MPPHRRKRPQINAKNFIPLYPOCSLSKEBSLSQALNTPINKKFKIKICRELAHEDGQPHH 60
QY 60 VLVQFEGKQYCTNNRPFEDIVSPTRSAHFHPNIOGAVSSDVYSYIDKQDPTIEMGFQID 119
Db 61 VLVQFEGKQYCTNNRPFEDIVSPTRSAHFHPNIOGAVSSDVYSYIDKQDPTIEMGFQID 120
QY 120 GSSAAGGQOSANDSVAKALNAGSVQSLALVREBQKDFLQONNINISNLERIPAKPEPW 179
Db 121 GSSAAGGQCTSDNDAEALNAGSKEBALQITREKITEKVLFOPHNLNLSNDRIFDKPEP 180
QY 180 WVPPEFQVSSFTVNPDEMOEWADNVPFGTDAAPDRPVSIIYEGDSRTGKTMMARALGPHN 239
Db 181 WLPPEHVSFTVNPDEMRQMAENYIPGKSSAARERISIIIEEDSRGKTMARSLGPHN 240
QY 240 YLSGHLDPNGRVFSSNDVOYNVIDIAPHYLKLKHWKELLGAQKQWQSNCKYKGPVQIKG 299
Db 241 YLSGHLDPNGRVFSSNEVEYNVIDIAPHYLKLKHWKELLGAQKQWQSNCKYKGPVQIKG 300
QY 300 IPATVLCNPGGASVYKFLDKAENTGLKNWTTIKNAIFITLTAPLYQESTQAS 351
Db 301 IPSIVLCNPGGASVYKFLDKAENTPLKNWTTIKNAIFVFLNSPLVQSSIOSS 352

RESULT 5
S28360
A:1 protein - beet curly top virus
C:Species: beet curly top virus
C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 09-Jul-2004

```

C:Accession: S28360
 R:Stanley, V.; Markham, P.G.; Callie, R.J.; Pinner, M.S.
 EMBL J. 5, 1761-1767, 1986
 A:Title: The nucleotide sequence of an infectious clone of the geminivirus beet curly top
 A:Reference number: S28360
 A:Accession: S28360
 A:Status: translation not shown
 A:molecule type: DNA
 A:Residues: 1-385 <STA>
 A:Cross-references: UNIPROT:Q39485; GB:M24597; EMBL:X04144; NID:G210678; PIDN:AAA42751.1
 C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 69.3%; Score 1344; DB 2; Length 385;
 Best Local Similarity 68.6%; Pred. No. 3e-96;
 Matches 242; Conservative 48; Mismatches 63; Indels 0; Gaps 0;

QY 1 MPPPKFRVQSKNYFLTYPOCSLSKEEALSQLONTNTPVKKFKIKICRELHENGEPHLHY 60
 DB 28 MPTTKFRIOAKNIFLTYPOCSLSKEEALSQLONTNTPVKKFKIKICRELHENGEPHLHY 87
 QY 61 LVQFEGKYQCTNNRFPDVSPTSAHFHPNIQGAASSDVKSYIDKDGDTIEWGDFQIDG 120
 DB 88 LIQFEGKYQCTNNRFPDVSPTSAHFHPNIQGAASSDVKSYIDKDGDTIEWGDFQIDG 147
 QY 121 RSARGGQGSANDSYAKALNAGVQSALAVLREOPDPVLYQNNIRSNLERIFAKAPEPW 180
 DB 148 RSARGGQGSANDSYAKALNAGVQSALAVLREOPDPVLYQNNIRSNLERIFAKAPEPW 207
 QY 181 VPPFQVSSFTNVDEMQEMADNFTGTDAAPDRPVSIIEGDSRTGKTMMARALGPNNY 240
 DB 208 TPLFPLSSTNVPEEMQEMADNFTGTDAAPDRPVSIIEGDSRTGKTMMARALGPNNY 267
 QY 241 LSGHLDENGRVSNVDVQNVNIDIAFHYLKLKHWKELGAQKQWQSNCKYKPEVQIKGGI 300
 DB 268 ITHGLDFSRVYDEEVNVDVQNVNIDIAFHYLKLKHWKELGAQKQWQSNCKYKPEVQIKGGI 327
 QY 301 PAIVLCNPEGASVYKFLDKAENTGLKNTIKNAIFITLPAFYQESTQASOE 353
 DB 328 PCLILCNPESSVYQFLKPEKNEALKSWTLNHTCKLQGLPLFNQAASSQ 380

RESULT 6

QY 301 PAIVLCNPEGASVYKFLDKAENTGLKNTIKNAIFITLPAFYQESTQASOE 353
 DB 328 PCLILCNPESSVYQFLKPEKNEALKSWTLNHTCKLQGLPLFNQAASSQ 380
 A:Title: protein - tomato yellow leaf curl virus (strain Australia)
 N:Alternate names: C1 protein
 C:Species: tomato yellow leaf curl virus
 C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
 C:Accession: J01887
 R:Idry, I.B.; Ridgen, J.E.; Krake, L.R.; Mullineaux, P.M.; Rezaian, M.A.
 J. Gen. Virol. 74, 147-151, 1993
 A:Title: Nucleotide sequence and genome organization of tomato leaf curl geminivirus.
 A:Reference number: J01885; NCID:93139778; PMID:8423446
 A:Accession: J01887
 A:Status: translation not shown
 A:molecule type: DNA
 A:Residues: 1-362 <DRY>
 A:Cross-references: UNIPROT:P36279; GB:S53251
 C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 69.1%; Score 1340.5; DB 1; Length 362;
 Best Local Similarity 69.8%; Pred. No. 5.2e-96;
 Matches 250; Conservative 43; Mismatches 56; Indels 9; Gaps 4;

QY 1 MPPPKFRVQSKNYFLTYPOCSLSKEEALSQLONTNTPVKKFKIKICRELHENGEPHLHY 60
 DB 1 MPTTKFRIOAKNIFLTYPOCSLSKEEALSQLONTNTPVKKFKIKICRELHENGEPHLHY 60
 QY 61 LVQFEGKYQCTNNRFPDVSPTSAHFHPNIQGAASSDVKSYIDKDGDTIEWGDFQIDG 120
 DB 61 LIQFEGKYQCTNNRFPDVSPTSAHFHPNIQGAASSDVKSYIDKDGDTIEWGDFQIDG 120
 QY 121 RSARGGQGSANDSYAKALNAGVQSALAVLREOPDPVLYQNNIRSNLERIFAKAPEPW 180
 DB 148 RSARGGQGSANDSYAKALNAGVQSALAVLREOPDPVLYQNNIRSNLERIFAKAPEPW 207

DB 121 RSARGGQGSANDSYAKALNAGVQSALAVLREOPDPVLYQNNIRSNLERIFAKAPEPW 180
 QY 181 VPPFQVSSFTNVPEEMQEMADNFTGTDAAPDRPVSIIEGDSRTGKTMMARALGPNNY 240
 DB 181 VSPFLSSSFDRVDEEELWVAENV--KDAAPRLPRLISIVIEGDSRTGKTMMARALGPNNY 238
 QY 240 YLSGHLDFNGRVSNVDVQNVNIDIAFHYLKLKHWKELGAQKQWQSNCKYKPEVQIKGGI 299
 DB 239 YLSGHLDFNGRVSNVDVQNVNIDIAFHYLKLKHWKELGAQKQWQSNCKYKPEVQIKGGI 296
 QY 300 PAIVLCNPEGASVYKFLDKAENTGLKNTIKNAIFITLPAFYQESTQASOE 353
 DB 297 IPTFLCNPESSVYQFLKPEKNEALKSWTLNHTCKLQGLPLFNQAASSQ 380

RESULT 7

QY 300 PAIVLCNPEGASVYKFLDKAENTGLKNTIKNAIFITLPAFYQESTQASOE 353
 DB 297 IPTFLCNPESSVYQFLKPEKNEALKSWTLNHTCKLQGLPLFNQAASSQ 380
 A:Title: Complete nucleotide of pepper huasteco virus: Analysis and comparison with bipar
 A:Reference number: JQ2299; NCID:94015007; PMID:8409944
 A:Accession: JQ2300
 A:molecule type: DNA
 A:Residues: 1-349 <TOR>
 A:Cross-references: UNIPROT:Q06923; GB:X70418; NID:G61023; PIDN:CAA49856.1; PID:G61025
 C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 69.0%; Score 1338.5; DB 2; Length 349;
 Best Local Similarity 67.9%; Pred. No. 7e-96;
 Matches 239; Conservative 53; Mismatches 55; Indels 5; Gaps 3;

QY 1 MPPPKFRVQSKNYFLTYPOCSLSKEEALSQLONTNTPVKKFKIKICRELHENGEPHLHY 60
 DB 1 MPTTKFRIOAKNIFLTYPOCSLSKEEALSQLONTNTPVKKFKIKICRELHENGEPHLHY 60
 QY 61 LVQFEGKYQCTNNRFPDVSPTSAHFHPNIQGAASSDVKSYIDKDGDTIEWGDFQIDG 120
 DB 61 LIQFEGKYQCTNNRFPDVSPTSAHFHPNIQGAASSDVKSYIDKDGDTIEWGDFQIDG 120
 QY 121 RSARGGQGSANDSYAKALNAGVQSALAVLREOPDPVLYQNNIRSNLERIFAKAPEPW 180
 DB 148 RSARGGQGSANDSYAKALNAGVQSALAVLREOPDPVLYQNNIRSNLERIFAKAPEPW 207
 QY 181 VPPFQVSSFTNVPEEMQEMADNFTGTDAAPDRPVSIIEGDSRTGKTMMARALGPNNY 240
 DB 181 VSPFLSSSFDRVDEEELWVAENV--KDAAPRLPRLISIVIEGDSRTGKTMMARALGPNNY 238
 QY 240 YLSGHLDFNGRVSNVDVQNVNIDIAFHYLKLKHWKELGAQKQWQSNCKYKPEVQIKGGI 299
 DB 239 YLSGHLDFNGRVSNVDVQNVNIDIAFHYLKLKHWKELGAQKQWQSNCKYKPEVQIKGGI 296
 QY 300 PAIVLCNPEGASVYKFLDKAENTGLKNTIKNAIFITLPAFYQESTQASOE 353
 DB 297 IPTFLCNPESSVYQFLKPEKNEALKSWTLNHTCKLQGLPLFNQAASSQ 380

RESULT 8

QY 300 PAIVLCNPEGASVYKFLDKAENTGLKNTIKNAIFITLPAFYQESTQASOE 353
 DB 297 IPTFLCNPESSVYQFLKPEKNEALKSWTLNHTCKLQGLPLFNQAASSQ 380
 A:Title: protein - pepper rizado amarillo virus
 N:Alternate names: ORF AL1 protein
 C:Species: pepper rizado amarillo virus
 C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
 C:Accession: S31875
 R:Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Jimenez, B.; Herrera-Betrelle, L.; Rivera-Bu
 submitted to the EMBL Data Library, February 1993
 A:Description: Complete nucleotide sequence of pepper huasteco virus: analysis and compa
 A:Reference number: S31872
 A:Accession: S31875
 A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-349 <TOR>
A:Cross-references: UNIPROT:Q06923; EMBL:X70418; NID:961023; PIDN:CAA49856.1; PID:961025
A>Note: the source is designated as pepper huasteco virus
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match
Best Local Similarity 67.6%; Score 1338.5; DB 2; Length 349;
Pred. No. 7e-96;
Matches 239; Conservative 53; Mismatches 55; Indels 5; Gaps 3;

QY 1 MPPPKKFRVQSKNYFLTYPCSSLSKEBALSQLQNLNTPVKKFKIKICREIHENGEPHLHY 60
DB 1 MPPPKKFRVQSKNYFLTYPCSSLSKEBALSQLQNLNTPVKKFKIKICREIHENGEPHLHY 60
QY 61 LVQFEGKYQCTNNRFPDLVSPTRSAHPHPIQAKSSDVKSYIDKDGDTIEMGDFOIDG 120
DB 61 LVQFEGKYQCTNNRFPDLVSPTRSAHPHPIQAKSSDVKSYIDKDGDTIEMGDFOIDG 120
QY 121 RSARGGQOQSANDSYAKALNAGVQSAALAVREBPQDFVLQNNHNSLRIEPAKAPPEW 180
DB 121 RSARGGQOQSANDSYAKALNAGVQSAALAVREBPQDFVLQNNHNSLRIEPAKAPPEW 180
QY 181 VPPFQVSSFTNVDEQEW-ADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMMARALGPHN 239
DB 181 VPPFQVSSFTNVDEQEW-ADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMMARALGPHN 239
QY 240 YLSGHLDFNGRVFENDVQVNVYIDIAHYLKLKMKWELLGAQKQWQSNCKYKGRVQIKGG 239
DB 239 YLSGHLDFNGRVFENDVQVNVYIDIAHYLKLKMKWELLGAQKQWQSNCKYKGRVQIKGG 239
QY 300 IPAIVLCNPEGASYSKEFLDKAENTGKKNWTIKNAIFITLTAFLYVSTOAS 351
DB 297 IPTIFLCNPEGASYSKEFLDKAENTGKKNWTIKNAIFITLTAFLYVSTOAS 348

RESULT 9

S22593
hypothetical protein C4 - tomato yellow leaf curl virus
C:Species: tomato yellow leaf curl virus
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S22593
R:Key:Pour, A.; Bendahmane, M.; Matzeit, V.; Accotto, G.P.; Crespi, S.; Gronenborn, B.
Nucleic Acids Res. 19, 6763-6769, 1991
A>Title: Tomato yellow leaf curl virus from Sardinia is a whitefly-transmitted monopartite
A:Reference number: S22588; MUID:92107660; PMID:1840676
A:Accession: S22593
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-359 <KHE>
A:Cross-references: UNIPROT:P27260; EMBL:X61153; NID:962211; PIDN:CAA43466.1; PID:962217
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match
Best Local Similarity 67.6%; Score 1311.5; DB 2; Length 359;
Pred. No. 8.9e-94;
Matches 240; Conservative 48; Mismatches 65; Indels 9; Gaps 4;

QY 1 MPPPKKFRVQSKNYFLTYPCSSLSKEBALSQLQNLNTPVKKFKIKICREIHENGEPHLHY 60
DB 1 MPPPKKFRVQSKNYFLTYPCSSLSKEBALSQLQNLNTPVKKFKIKICREIHENGEPHLHY 60
QY 61 LVQFEGKYQCTNNRFPDLVSPTRSAHPHPIQAKSSDVKSYIDKDGDTIEMGDFOIDG 120
DB 61 LVQFEGKYQCTNNRFPDLVSPTRSAHPHPIQAKSSDVKSYIDKDGDTIEMGDFOIDG 120
QY 121 RSARGGQOQSANDSYAKALNAGVQSAALAVREBPQDFVLQNNHNSLRIEPAKAPPEW 180
DB 121 RSARGGQOQSANDSYAKALNAGVQSAALAVREBPQDFVLQNNHNSLRIEPAKAPPEW 180
QY 181 VPPFQVSSFTNVDEQEW-ADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMMARALGPHN 239
DB 181 VPPFQVSSFTNVDEQEW-ADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMMARALGPHN 239

QY 240 YLSGHLDFNGRVFENDVQVNVYIDIAHYLKLKMKWELLGAQKQWQSNCKYKGRVQIKGG 239
DB 239 YLSGHLDFNGRVFENDVQVNVYIDIAHYLKLKMKWELLGAQKQWQSNCKYKGRVQIKGG 236
QY 300 IPAIVLCNPEGASYSKEFLDKAENTGKKNWTIKNAIFITLTAFLYVSTOAS 355
DB 297 IPTIFLCNPEGASYSKEFLDKAENTGKKNWTIKNAIFITLTAFLYVSTOAS 356

QY 356 NQ 357
DB 357 SE 358

RESULT 10

S59885
replication-associated protein C1 - tomato yellow leaf curl virus
C:Species: tomato yellow leaf curl virus
C>Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C/Accession: S59885
R:Hong, Y.; Harrison, B.D.
submitted to the EMBL Data Library, February 1995
A>Description: Nucleotide sequences from tomato leaf curl viruses from different countries
d geminiviruses.
A:Reference number: S59885
A:Accession: S59885
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-360 <HON>
A:Cross-references: UNIPROT:Q08557; EMBL:Z48182; NID:9944838; PIDN:CAA88229.1; PID:997423
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match
Best Local Similarity 67.6%; Score 1310.5; DB 2; Length 360;
Pred. No. 1.1e-93;
Matches 244; Conservative 46; Mismatches 62; Indels 9; Gaps 4;

QY 1 MPPPKKFRVQSKNYFLTYPCSSLSKEBALSQLQNLNTPVKKFKIKICREIHENGEPHLHY 60
DB 1 MPPPKKFRVQSKNYFLTYPCSSLSKEBALSQLQNLNTPVKKFKIKICREIHENGEPHLHY 60
QY 61 LVQFEGKYQCTNNRFPDLVSPTRSAHPHPIQAKSSDVKSYIDKDGDTIEMGDFOIDG 120
DB 61 LVQFEGKYQCTNNRFPDLVSPTRSAHPHPIQAKSSDVKSYIDKDGDTIEMGDFOIDG 120
QY 121 RSARGGQOQSANDSYAKALNAGVQSAALAVREBPQDFVLQNNHNSLRIEPAKAPPEW 180
DB 121 RSARGGQOQSANDSYAKALNAGVQSAALAVREBPQDFVLQNNHNSLRIEPAKAPPEW 180
QY 181 VPPFQVSSFTNVDEQEWADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMMARALGPHN 240
DB 181 VPPFQVSSFTNVDEQEWADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMMARALGPHN 240
QY 241 LSGHLDFNGRVFENDVQVNVYIDIAHYLKLKMKWELLGAQKQWQSNCKYKGRVQIKGG 300
DB 239 LSGHLDFNGRVFENDVQVNVYIDIAHYLKLKMKWELLGAQKQWQSNCKYKGRVQIKGG 296
QY 301 PAIVLCNPEGASYSKEFLDKAENTGKKNWTIKNAIFITLTAFLYVSTOAS 356
DB 297 IPTIFLCNPEGASYSKEFLDKAENTGKKNWTIKNAIFITLTAFLYVSTOAS 355

RESULT 11

JQ2327
AL1 protein - Indian cassava mosaic virus
N:Alternate names: replication-associated protein
C:Species: Indian cassava mosaic virus
C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C/Accession: JQ2327; S35883
R:Hong, Y.G.; Robinson, D.J.; Harrison, B.D.
J. Gen. Virol. 74, 2437-2443, 1993

A>Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-tran
A/Reference number: JQ2326; MID:94065670; PMID:8245859
A/Accession: JQ2327
A/Molecule type: DNA
A/Residues: 1-351 <HON>
A/Cross-references: UNIPROT:Q82676; EMBL:Z24758; NID:g395351; PIDD:CAA80891.1; PID:g5840
C/Superfamily: tomato golden mosaic virus AL1 protein

Query Match 67.4%; Score 1307; DB 2; Length 351;
Best Local Similarity 67.6%; Pred. No. 1.9e-93;
Matches 240; Conservative 43; Mismatches 66; Indels 6; Gaps 3;

QY 1 MPPPKRVSQKNYFLTYPCSLSKKEALSOLOLNTPVNKKTKICREIHENGEPHLAV 60
DB 1 MSPPKRFQINAKYFLTYPCSLSKKEALSOLOLNTPVNKKTKICREIHENGEPHLAV 60
QY 61 LVPEKGYOCTNNRFPDLVSPTRSAHPHNIQAKSSSDVYSYIDKDGDTIEMGDFQIDG 120
DB 61 LVPEKGYOCTNNRFPDLVSPTRSAHPHNIQAKSSSDVYSYIDKDGDTIEMGDFQIDG 120
QY 121 RSARGGQOSANDSYAKALNAGVOSALAVREBPQDFVLQNNHNSLRIEPAKAPPEW 180
DB 121 RSARGGQOSANDSYAKALNAGVOSALAVREBPQDFVLQNNHNSLRIEPAKAPPEW 180
QY 121 RSARGGQOSANDSYAKALNAGVOSALAVREBPQDFVLQNNHNSLRIEPAKAPPEW 180
DB 121 RSARGGQOSANDSYAKALNAGVOSALAVREBPQDFVLQNNHNSLRIEPAKAPPEW 180
QY 181 VPPFQVSSFTNVDEMOEW-ADNYFGTGDAAPDPSPVSIIVEGDSRTGKTMARALGPHN 239
DB 181 ENPFPLSSFDVBELEDEWFHEHVMG--RARPRLPKSVIIEGDSRTGKTMARALGPHN 237
QY 240 YLSGHLDFNGRVPSNDVQNVVIDIAPHYLKLMKMKELGAQKQWQSNCKYKGPVOIKGG 239
DB 238 YLGGHLDLSPKRYVNDAMVNVIDVDPHY--LKHFKIHGGPEQWQSNCKYKGPVOIKGG 235
QY 300 IPAIVLCNPEGASVKEFLDKAENTGLKNMTIKNAIFITLTAPLYOBSTQASOET 354
DB 296 IPTPLCNPEPNSYKEFLDEEKNSALKAMALKNAITISLEGPLYSTNGPTQGS 350

RESULT 12

gene C1 protein - tomato yellow leaf curl virus
S39211
C/Species: tomato yellow leaf curl virus
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C/Accession: S39211
R/Norris, E.; Hidalgo, E.; Accotto, G.; Moriones, E.
submitted to the EMBL Data Library, August 1993
A/Description: High similarity among the tomato yellow leaf curl virus isolates from the
A/Reference number: S39209
A/Accession: S39211
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-359 <NOR>
A/Cross-references: UNIPROT:P38609; EMBL:Z25751; NID:g433655; PIDD:CAA01026.1; PID:g4336
C/Superfamily: tomato golden mosaic virus AL1 protein

Query Match 67.3%; Score 1305.5; DB 2; Length 359;
Best Local Similarity 67.1%; Pred. No. 2.6e-93;
Matches 235; Conservative 52; Mismatches 58; Indels 5; Gaps 3;

QY 1 MPPPKRVSQKNYFLTYPCSLSKKEALSOLOLNTPVNKKTKICREIHENGEPHLAV 60
DB 1 MAOPKRFQINAKYFLTYPCSLSKKEALSOLOLNTPVNKKTKICREIHENGEPHLAV 60
QY 61 LVPEKGYOCTNNRFPDLVSPTRSAHPHNIQAKSSSDVYSYIDKDGDTIEMGDFQIDG 120
DB 61 LVPEKGYOCTNNRFPDLVSPTRSAHPHNIQAKSSSDVYSYIDKDGDTIEMGDFQIDG 120
QY 121 RSARGGQOSANDSYAKALNAGVOSALAVREBPQDFVLQNNHNSLRIEPAKAPPEW 180
DB 121 RSARGGQOSANDSYAKALNAGVOSALAVREBPQDFVLQNNHNSLRIEPAKAPPEW 180
QY 181 VPPFQVSSFTNVDEMOEW-ADNYFGTGDAAPDPSPVSIIVEGDSRTGKTMARALGPHN 239
DB 181 VSEFPLSSFDVBELEDEHVMVSENYMDA--AARPRPVSIIVEGDSRTGKTMARALGPHN 238

QY 240 YLSGHLDFNGRVPSNDVQNVVIDIAPHYLKLMKMKELGAQKQWQSNCKYKGPVOIKGG 239
DB 239 YLGGHLDLSPKRYVNDAMVNVIDVDPHY--LKHFKIHGGPEQWQSNCKYKGPVOIKGG 236
QY 300 IPAIVLCNPEGASVKEFLDKAENTGLKNMTIKNAIFITLTAPLYOBSTQ 349
DB 297 IPTPLCNPEPNSYKEFLDEEKNSALKAMALKNAITISLEGPLYSTNGPTQGS 346

RESULT 13

QGCCYC1
AL1 protein - tomato yellow leaf curl virus
N/Alternate names: C1 protein
C/Species: tomato yellow leaf curl virus
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C/Accession: D40779
R/Navot, N.; Pichereky, E.; Zeidan, M.; Zambir, D.; Czosnek, H.
Virology 185, 151-161, 1991
A>Title: Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus with a single
A/Reference number: A40779; MID:92024070; PMID:1926771
A/Accession: D40779
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-357 <NAV>
A/Cross-references: UNIPROT:P27259; GB:X15656; NID:g62204; PIDD:CAA33688.1; PID:g62207
C/Superfamily: tomato golden mosaic virus AL1 protein

Query Match 66.9%; Score 1296.5; DB 1; Length 357;
Best Local Similarity 66.6%; Pred. No. 1.3e-92;
Matches 239; Conservative 52; Mismatches 59; Indels 9; Gaps 4;

QY 4 PKKRVOSKNYFLTYPCSLSKKEALSOLOLNTPVNKKTKICREIHENGEPHLAV 63
DB 2 PRFKYIYANKYFLTYPCSLSKKEALSOLOLNTPVNKKTKICREIHENGEPHLAV 61
QY 64 FEKRYOCTNNRFPDLVSPTRSAHPHNIQAKSSSDVYSYIDKDGDTIEMGDFQIDG 123
DB 62 FEKRYOCTNNRFPDLVSPTRSAHPHNIQAKSSSDVYSYIDKDGDTIEMGDFQIDG 121
QY 124 RGGQOSANDSYAKALNAGVOSALAVREBPQDFVLQNNHNSLRIEPAKAPPEW 183
DB 122 RGGQOSANDSYAKALNAGVOSALAVREBPQDFVLQNNHNSLRIEPAKAPPEW 181
QY 184 FQVSEFTNVDEMOEW-ADNYFGTGDAAPDPSPVSIIVEGDSRTGKTMARALGPHN 242
DB 182 FLSSSTNVQVDELEHVAENV--VSAARPMWRISIVIEGDSRTGKTMARALGPHN 239
QY 243 GHLDLDFNGRVPSNDVQNVVIDIAPHYLKLMKMKELGAQKQWQSNCKYKGPVOIKG 302
DB 240 GHLDLDFNGRVPSNDVQNVVIDIAPHYLKLMKMKELGAQKQWQSNCKYKGPVOIKG 297
QY 303 IYLCNPEGASVKEFLDKAENTGLKNMTIKNAIFITLTAPLY-----QESTQASOETG 357
DB 298 IFLCNPEGASVKEFLDKAENTGLKNMTIKNAIFITLTAPLY-----QESTQASOETG 356

RESULT 14

S39235
gene C1 protein - tomato yellow leaf curl virus
C/Species: tomato yellow leaf curl virus
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C/Accession: S39235
R/Crespi, S.; Norris, E.; Valira, A.; Bosco, D.; Accotto, G.
submitted to the EMBL Data Library, December 1993
A/Description: A cloned DNA from a TYLCV isolate from Sicily showing low infectivity.
A/Reference number: S39233
A/Accession: S39235
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-359 <CRE>
A/Cross-references: UNIPROT:Q88949; EMBL:Z28390; NID:g1041671; PID:g1334964
C/Superfamily: tomato golden mosaic virus AL1 protein

Query Match 66.6%; Score 1290.5; DB 2; Length 359;
 Best Local Similarity 64.5%; Pred. No. 3.7e-92;
 Matches 234; Conservative 56; Mismatches 64; Indels 9; Gaps 4;

```

QY 1 MPPKFERVOSKNVFLTYQCSLSKEBALSQLNTLPVKKFKIKICREIHENGEPHLAV 60
DB 1 MAGPKRQINAKHYFLTFPPKCCULKEALBGLTLQPTNKXYIKICREIHEDGQPLHI 60
QY 61 LVQPEGKYQCTNNRFFFLVSPTRSAHFHFNIOGAKSSDVKSYIDKQGDITTEKQDFQIDG 120
DB 61 LMQFEGKFNCKNNRFFFLVSPTRSAHFHFNIOGAKSSDVKSYIDKQGDVLEWETFOIDG 120
QY 121 RSARGGQGSANDSYAKALNAGSVQSLAVLREBPQDFVLQNHNRISNLERIFAKAPEPW 180
DB 121 RSARGGQGITNDAYAKALNAGSVQSLAVLREBPQDFVLQNHNRISNLERIFQVPPAPY 180
QY 181 VPPFOVSSFTNVDPDEMEW-ADNYFGTGDAAPDPDPVSIIVEGDSRTGKTMMARALGPHN 239
DB 181 VSPFLSSFPQVPELEHWTSENMDV--AARPMRPVSIIVEGDSRTGKTMMARSLGPHN 238
QY 240 YLSGHLDPNGRVSNVDQVNVIDIAHYTLKHKWKELLGAQKDQWQSNCKYKQPVQIKG 299
DB 239 YLGGHLDLSQKVSNNAMVNVIDVDPHY--LKHFKEFMGAQRDMQNTYKQKPIQIKG 296
QY 300 IPAIVLCNPGEGASYKEFLDKAENTGKKNWTKKNAIFITLTAPLY---QESTQASQETG 355
DB 297 IPTIFLCNPGPOSSFKEYLDEBKQALKNNAIKNAIFITIDQPLFTDTHQNTTPHROEA 356
QY 356 NQK 358
DB 357 GEE 359

```

RESULT 15

S07594
 hypothetical protein, 40.4K - cassava latent virus (Nigerian isolate)
 C:Species: cassava latent virus
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C:Accession: S07594
 R:Morris, B.; Coates, L.; Lowe, S.; Richardson, K.; Eddy, P.
 Nucleic Acids Res. 18, 197-198, 1990
 A:Title: Nucleotide sequence of the infectious cloned DNA components of African cassava
 A:Reference number: S07590; MUID:90174930; PMID:2308831
 A:Accession: S07594
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-358 <MOR>
 A:Cross-references: UNIPROT:P14972; EMBL:X17095; NID:G59371; PIDN:CAA34953.1; PID:G59376
 C:Genetic:
 A:Map position: segment DNA1
 C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 66.1%; Score 1282.5; DB 2; Length 358;
 Best Local Similarity 68.6%; Pred. No. 1.6e-91;
 Matches 240; Conservative 38; Mismatches 67; Indels 5; Gaps 3;

```

QY 6 KFRVQSNVFLTYQCSLSKEBALSQLNTLPVKKFKIKICREIHENGEPHLAVQPE 65
DB 5 RFRVQAKNVFLTYPNCSIPKHEHLSFTQTLSPENPKFIKICREIHONGEPHLALQFE 64
QY 66 GKYOCTNNRFFFDLVSPTRSAHFHFNIOGAKSSDVKSYIDKQGDITTEKQDFQIDGRSARG 125
DB 65 GKTTITNNRFLPDCVHPSCSTNRFHFNIOGAKSSDVKSYLDKQDPTVEMGQFQIDGRSARG 124
QY 126 GQGSANDSYAKALNAGSVQSLAVLREBPQDFVLQNHNRISNLERIFAKAPEWVPPFQ 185
DB 125 GQGSANDAYAKALNAGSVQSLAVLREBPQDFVLQNHNRISNLERIFQBPAPVYVGF 184
QY 186 VSGFTNVDPDEMEW-ADNYFGTGDAAPDPDPVSIIVEGDSRTGKTMMARALGPHNYLSG 244
DB 185 CSSFQDVYDELEWADVNV--RDSAPRPWPNISIVIGDSRTGKTIVARSIGPHNYLGGH 242

```

```

QY 245 LDFNGRVFSNDVQVNVIDIAHYTLKHKWKELLGAQKDQWQSNCKYKQPVQIKGIPAI 304
DB 243 LDISPKVFNNDAMVNVIDVDPHY--LKHFKEFMGAQRDMQNTYKQKPIQIKGIPITIF 300
QY 305 LCNPGEGASYKEFLDKAENTGKKNWTKKNAIFITLTAPLYQESTQASQET 354
DB 301 LCNPGPTSSYKEFLDEBKQALKNNAIKNAIFITLTPFLYSGSNOSQRT 350

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Search completed: December 3, 2004, 15:01:43
 Job time : 50 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2004, 14:55:20 ; Search time 193 Seconds

(Without alignments)
1076.219 Million cell updates/sec

Title: US-09-491-063a-2

Sequence: 1 MPPPKFRVQSKNYFLTPQ.....PLYQESTQASQETGNGKAG 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1939	100.0	361	1 VAL1.TMOV	O06657 tomato mot
2	1908	98.4	361	2 Q67614	Q67614 tomato mot
3	1792	92.4	361	2 O71963	O71963 sida golden
4	1764	91.0	356	2 O11842	O11842 abutillon mo
5	1736	89.5	361	2 Q9YL74	Q9YL74 chino del t
6	1731	89.3	361	2 Q7HTH9	Q7HTH9 tomato mot
7	1722	88.8	361	2 Q36624	Q36624 tomato mot
8	1715	88.4	361	2 Q9J051	Q9J051 chino del t
9	1711	88.2	361	2 Q96612	Q96612 abutillon mo
10	1710	88.2	361	2 Q9J049	Q9J049 chino del t
11	1690	87.2	361	2 P89127	P89127 sida yellow
12	1689	87.1	361	2 Q8JUV1	Q8JUV1 tobacco lea
13	1664	85.8	361	2 Q67558	Q67558 bean dwarf
14	1652	85.2	350	2 Q71205	Q71205 potato yell
15	1640	84.6	361	2 P89122	P89122 sida golden
16	1635.5	84.3	360	2 Q9YVW9	Q9YVW9 sida golden
17	1606	82.8	358	2 Q91201	Q91201 tomato mosa
18	1597.5	82.4	360	2 Q9YVW5	Q9YVW5 sida golden
19	1596	82.4	348	2 Q911W5	Q911W5 macroptiliu
20	1585	81.7	353	2 Q9QGH3	Q9QGH3 bean golden
21	1582	81.6	353	2 Q80P44	Q80P44 bean golden
22	1575	81.2	353	2 P87726	P87726 bean golden
23	1572	81.1	353	2 Q01731	Q01731 bean golden
24	1572	81.1	361	2 VAL1.PYVW	P27258 potato yell
25	1569	80.9	351	2 Q41339	Q41339 potato yell
26	1566	80.8	361	2 Q8JMW4	Q8JMW4 potato yell
27	1562	80.6	355	1 VAL1.ABWW	P21947 abutillon mo
28	1557.5	80.3	351	2 Q78V7	Q78V7 sida golden
29	1549	79.9	351	2 Q9Q9R3	Q9Q9R3 dicliptera
30	1547	79.8	353	1 VAL1.BGVV	P51175 bean golden
31	1527	78.8	351	2 Q8QR22	Q8QR22 tomato chlo

ALIGNMENTS

32	1523	78.5	351	2	Q801H6	O801H6 dicliptera
33	1522	78.5	358	2	Q70PB5	Q70PB5 sida micran
34	1522	78.5	358	2	CAD89709	CAD89709 sida micr
35	1516	78.2	358	2	Q6R7R5	Q6R7R5 tomato mosa
36	1516	78.2	358	2	AAR95968	AAR95968 tomato mo
37	1512	78.0	344	2	Q6R7Q8	Q6R7Q8 tomato yell
38	1512	78.0	344	2	AAR95975	AAR95975 tomato ye
39	1502.5	77.5	352	1	VAL1.TGMV	P03657 tomato gold
40	1498	77.3	361	2	Q67574	Q67574 bean golden
41	1497.5	77.2	349	2	Q8JUNH1	Q8JUNH1 macroptiliu
42	1493	77.0	346	2	Q7TSV0	Q7TSV0 tomato chin
43	1489.5	76.8	352	2	Q8QW6	Q8QW6 tomato chlo
44	1483	76.5	352	2	Q9E0C0	Q9E0C0 tomato rugo
45	1470	75.8	358	2	Q70PC0	Q70PC0 sida micran

RESULT 1

VAL1.TMOV	STANDARD;	PRT;	361 AA.
ID	VAL1.TMOV		
AC	O06657;		
DT	01-JUN-1994 (Rel. 29, Created)		
DT	01-JUN-1994 (Rel. 29, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	ALI protein.		
GN	Name=ALI;		
OS	Tomato mottle virus (isolate Florida) (TMOV).		
OC	Virusess; ssDNA viruses; Geminiviridae; Begomovirus.		
OX	NCBI_TaxID=36449;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=93107858; PubMed=1469361;		
RA	Abouid A.M., Polston J.E., Hiebert B.;		
RT	"The nucleotide sequence of tomato mottle virus, a new geminivirus isolated from tomatoes in Florida."		
RL	J. Gen. Virol. 73:3225-3229(1992).		
CC	-1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).		
CC	EMBL: L14460; AAC32414.1; -.		
DR	PIR; JQ1870; JQ1870.		
DR	HSSP; P27260; 1L51.		
DR	InterPro; IPR001191; Gemin1 AL1.		
DR	InterPro; IPR001301; Gemin1 AL1_CLV.		
DR	Pfam; PF00799; Gemin1 AL1; I.		
DR	PRINTS; PR00227; GEMCATAL1.		
DR	PRINTS; PR00228; GEMCATCLV1.		
DR	ProDom; PD000736; Gemin1_AL1; 1.		
KW	ATP-binding.		
FT	NP BIND 222		
FT	NP BIND 229		
SQ	SEQUENCE 361 AA; 40516 MW; 813865CCEAC6950 CRC64;		

Query Match 100.0%; Score 1939; DB 1; Length 361;
Best Local Similarity 100.0%; Pred. No. 4,5e-143;
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MPPPKFRVQSKNYFLTPQCSLSKEALSQLONTLPVKKRIRIKICRELAHNGEPHLV	60
DB	1	MPPPKFRVQSKNYFLTPQCSLSKEALSQLONTLPVKKRIRIKICRELAHNGEPHLV	60
QY	61	LVOFEGKYCTNNRFPDLVSPTRSAHFPHNIQCAKSSDVKSYIDKGGTIEWGDFQIDG	120
DB	61	LVOFEGKYCTNNRFPDLVSPTRSAHFPHNIQCAKSSDVKSYIDKGGTIEWGDFQIDG	120

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QY 121 RSARGGQOSANDSYAKALNAGSVOSALAVLREEQPKDFVLQNNHNRSLERIFAKAPEPW 180
  |||
Db 121 RSARGGQOSANDSYAKALNAGSVOSALAVLREEQPKDFVLQNNHNRSLERIFAKAPEPW 180
QY 181 VPPFQVSSFTNVDPDEQEMADNFTGTGDAAPDRPVSIIYEGDSRTGKTMMARALGPHNY 240
  |||
Db 181 VPPFQVSSFTNVDPDEQEMADNFTGTGDAAPDRPVSIIYEGDSRTGKTMMARALGPHNY 240
QY 241 LSGHLDNFGVFSNDVQYNYIDIDIAPHYLLKHKMKELGAKQKQMSCKTKGKPVQIKGGI 300
  |||
Db 241 LSGHLDNFGVFSNDVQYNYIDIDIAPHYLLKHKMKELGAKQKQMSCKTKGKPVQIKGGI 300
QY 301 PAIVLCNPGEGASKEFLDRAENTGLKNWTKIKNAIFITLTPAPLYQESTQASQETGNQKQ 360
  |||
Db 301 PAIVLCNPGEGASKEFLDRAENTGLKNWTKIKNAIFITLTPAPLYQESTQASQETGNQKQ 360
QY 361 G 361
  |||
Db 361 G 361

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RESULT 2

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ID Q67614 PRELIMINARY; PRT; 361 AA.
AC Q67614;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Replicative protein.
GN Name=Al1;
OS Tomato mottle virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10835;
RN [1]
RP SEQUENCE FROM N.A.
RA Gibeleson R.L., Hidayat S.H., Rojars M.R., Maxwell D.P.;
RT "Infectious DNA clones of a new geminivirus associated with tomatoes in Florida."
RL Phytopathology 81:1184-1184(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93139780; PubMed=8423448;
RA Gibeleson R.L., Hidayat S.H., Rojars M.R., Hou Y.M., Maxwell D.P.;
RT "Pseudorecombination between infectious cloned DNA components of tomato mottle and bean dwarf mosaic geminiviruses."
RL J. Gen. Virol. 74:23-31(1993).
CC -1- SIMILARITY: Belongs to the geminiviruses Al1 protein family.
DR EMBL; M90495; AAA02942.1; -.
DR HSSP; P27260; 1L51.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR001191; Gemin1 Al1.
DR InterPro; IPR001301; Gemin1 Al1_CLV.
DR Pfam; PF00799; Gemin1 Al1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR PRINTS; PR00228; GEMCOATL1.
DR ProDom; PD000736; Gemin1 Al1; 1.
SQ SEQUENCE 361 AA; 40547 MW; 3B3B2F75099A293C CRC64;

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Query Match 98.4%; Score 1908; DB 2; Length 361;
Best Local Similarity 98.3%; Pred. No. 1.2e-140;
Matches 355; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY 1 MPPPKRRVQSKYVFLTYPCOSLSKEBALSQLQNLNTPVKKFKIKREIHENGEPHLAV 60
  |||
Db 1 MPPPKRRVQSKYVFLTYPCOSLSKEBALSQLQNLNTPVKKFKIKREIHENGEPHLAV 60
QY 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVKSYIDKGDITVEGDPQIDG 120
  |||
Db 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVKSYIDKGDITVEGDPQIDG 120
QY 121 RSARGGQOSANDSYAKALNAGSVOSALAVLREEQPKDFVLQNNHNRSLERIFAKAPEPW 180

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Db 121 RSARGGQOSANDSYAKALNAGSVOSALAVLREEQPKDFVLQNNHNRSLERIFAKAPEPW 180
  |||
QY 181 VPPFQVSSFTNVDPDEQEMADNFTGTGDAAPDRPVSIIYEGDSRTGKTMMARALGPHNY 240
  |||
Db 181 VPPFQVSSFTNVDPDEQEMADNFTGTGDAAPDRPVSIIYEGDSRTGKTMMARALGPHNY 240
QY 241 LSGHLDNFGVFSNDVQYNYIDIDIAPHYLLKHKMKELGAKQKQMSCKTKGKPVQIKGGI 300
  |||
Db 241 LSGHLDNFGVFSNDVQYNYIDIDIAPHYLLKHKMKELGAKQKQMSCKTKGKPVQIKGGI 300
QY 301 PAIVLCNPGEGASKEFLDRAENTGLKNWTKIKNAIFITLTPAPLYQESTQASQETGNQKQ 360
  |||
Db 301 PAIVLCNPGEGASKEFLDRAENTGLKNWTKIKNAIFITLTPAPLYQESTQASQETGNQKQ 360
QY 361 G 361
  |||
Db 361 G 361

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RESULT 3

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ID O71963 PRELIMINARY; PRT; 361 AA.
AC O71963;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Replication associated protein.
GN Name=AC1;
OS Sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51034;
RN [1]
RP SEQUENCE FROM N.A.
RA Abouzid A.M., Polston J.E., Hiebert E.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the geminiviruses Al1 protein family.
DR EMBL; AF049336; AAC05152.1; -.
DR HSSP; P27260; 1L51.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR001191; Gemin1 Al1.
DR InterPro; IPR001301; Gemin1 Al1_CLV.
DR Pfam; PF00799; Gemin1 Al1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR PRINTS; PR00228; GEMCOATL1.
DR ProDom; PD000736; Gemin1 Al1; 1.
SQ SEQUENCE 361 AA; 40678 MW; 57FA4DF1A86DD637 CRC64;

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Query Match 92.4%; Score 1792; DB 2; Length 361;
Best Local Similarity 91.1%; Pred. No. 1.4e-131;
Matches 328; Conservative 20; Mismatches 12; Indels 0; Gaps 0;

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QY 1 MPPPKRRVQSKYVFLTYPCOSLSKEBALSQLQNLNTPVKKFKIKREIHENGEPHLAV 60
  |||
Db 1 MPPPKRRVQSKYVFLTYPCOSLSKEBALSQLQNLNTPVKKFKIKREIHENGEPHLAV 60
QY 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVKSYIDKGDITVEGDPQIDG 120
  |||
Db 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVKSYIDKGDITVEGDPQIDG 120
QY 121 RSARGGQOSANDSYAKALNAGSVOSALAVLREEQPKDFVLQNNHNRSLERIFAKAPEPW 180
  |||
Db 121 RSARGGQOSANDSYAKALNAGSVOSALAVLREEQPKDFVLQNNHNRSLERIFAKAPEPW 180
QY 181 VPPFQVSSFTNVDPDEQEMADNFTGTGDAAPDRPVSIIYEGDSRTGKTMMARALGPHNY 240
  |||
Db 181 VPPFQVSSFTNVDPDEQEMADNFTGTGDAAPDRPVSIIYEGDSRTGKTMMARALGPHNY 240
QY 241 LSGHLDNFGVFSNDVQYNYIDIDIAPHYLLKHKMKELGAKQKQMSCKTKGKPVQIKGGI 300
  |||
Db 241 LSGHLDNFGVFSNDVQYNYIDIDIAPHYLLKHKMKELGAKQKQMSCKTKGKPVQIKGGI 300

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QY 301 PAIVLCNPGSGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYOESTQASOETGNOKAQ 360
 DB 301 PAIVLCNPGSGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYOESTQASOEGHTEAE 360

RESULT 4

ID 011842 PRELIMINARY; PRT; 356 AA.
 AC 011842;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE 40.2 kDa.
 GN Name=ORF C1;
 OS Abutillon mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxId=10815;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=91020984; PubMed=2219703;
 RX Frieschmuth T., Zimmat G., Jeske H.;
 RT "The nucleotide sequence of the abutillon mosaic virus reveals
 RT prokaryotic as well as eukaryotic features."
 RL Virology 178:461-468(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Jeske H.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
 DR EMBL; X15983; CAA34111.2; -;
 DR GO; GO:0019028; C: viral capsid; IEA.
 DR GO; GO:0005198; F: structural molecule activity; IEA.
 DR InterPro; IPR001191; Gemini_AL1.
 DR Pfam; PF00799; Gemini_AL1; CLV.
 DR PRINTS; PR00227; GEMCOATLVL.
 DR PRINTS; PR00228; GEMCOATLVL.
 DR ProDom; PD000736; Gemini_AL1.1.
 DR CHAIN 333 356 14.4 kDa.
 SQ SEQUENCE 356 AA; 40247 MW; 3AA732F65867352A CRC64;

Query Match 91.0%; Score 1764; DB 2; Length 356;
 Best Local Similarity 89.6%; Pred. No. 2.1e-129;
 Matches 319; Conservative 24; Mismatches 13; Indels 0; Gaps 0;

QY 1 MPPPKFRVQSKYKFLTYPCQSLSKKEALSQLONTLPVNNKFKIKICREIHENGEPHLHY 60
 DB 1 MPPPKFRVQSKYKFLTYPCQSLSKKEALSQLONTLPVNNKFKIKICREIHENGEPHLHY 60
 QY 61 LVQFEKRYQCTNNRFPDLVSPTRSAHFHPNIOGAKSSSDVKSYYIDKGDTEIEMGDFQIDG 120
 DB 61 LVQFEKRYQCTNNRFPDLVSPTRSAHFHPNIOGAKSSSDVKSYYIDKGDTEIEMGDFQIDG 120
 QY 121 RSARGGQGSANDSYAALNAGSVQSAALVREOPKDFVLONHNIRSNLERIFAKAPEPW 180
 DB 121 RSARGGQGSANDSYAALNAGSVQSAALVREOPKDFVLONHNIRSNLERIFAKAPEPW 180
 QY 181 VPPFOVSSFTNVDEMQEMADNYFGTGDAAAPPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
 DB 181 VPPFOVSSFTNVDEMQEMADNYFGTGDAAAPPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
 QY 241 LSGHLDPNRGRVPSNDVQVNVIDIAHYLTKLKWKEKLLGAQKQWQSNCKYKGRVQIKGCI 300
 DB 241 LSGHLDPNRGRVPSNDVQVNVIDIAHYLTKLKWKEKLLGAQKQWQSNCKYKGRVQIKGCI 300
 QY 301 PAIVLCNPGSGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYOESTQASOETGN 356
 DB 301 PAIVLCNPGSGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYOESTQASOEGH 356

RESULT 5
 Q9YL74 PRELIMINARY; PRT; 361 AA.
 ID Q9YL74

AC Q9YL74;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE AC1 protein.
 OS Chino del tomate virus-[IC].
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxId=222455;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jiang H., Hou Y.-M., Guzman P., Gilbertson R.L.;
 RT "Complete nucleotide sequence of the infectious clone of tomato leaf
 RT crumple geminivirus."
 RL (in) Unknown A. (eds.);
 RL ANNUAL MEETING OF THE AMERICAN PHYTOPATHOLOGICAL SOCIETY,
 RL PHYTOPATHOLOGY, VOL 88 (SUPPL), pp.44-0, Unknown publisher (1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RA Jiang H., Hou Y.-M., Guzman P., Gilbertson R.L.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
 DR EMBL; AF101476; AAD17898.1; -;
 DR HSSP; P27260; 1L5I.
 DR GO; GO:0019028; C: viral capsid; IEA.
 DR GO; GO:0005198; F: structural molecule activity; IEA.
 DR InterPro; IPR001191; Gemini_AL1.
 DR Pfam; PF00799; Gemini_AL1; CLV.
 DR PRINTS; PR00227; GEMCOATLVL.
 DR PRINTS; PR00228; GEMCOATLVL.
 DR ProDom; PD000736; Gemini_AL1.1.
 SQ SEQUENCE 361 AA; 40826 MW; 7968527DD3A185B1 CRC64;

Query Match 89.5%; Score 1736; DB 2; Length 361;
 Best Local Similarity 88.3%; Pred. No. 3.3e-127;
 Matches 316; Conservative 25; Mismatches 17; Indels 0; Gaps 0;

QY 1 MPPPKFRVQSKYKFLTYPCQSLSKKEALSQLONTLPVNNKFKIKICREIHENGEPHLHY 60
 DB 1 MPPPKFRVQSKYKFLTYPCQSLSKKEALSQLONTLPVNNKFKIKICREIHENGEPHLHY 60
 QY 61 LVQFEKRYQCTNNRFPDLVSPTRSAHFHPNIOGAKSSSDVKSYYIDKGDTEIEMGDFQIDG 120
 DB 61 LVQFEKRYQCTNNRFPDLVSPTRSAHFHPNIOGAKSSSDVKSYYIDKGDTEIEMGDFQIDG 120
 QY 121 RSARGGQGSANDSYAALNAGSVQSAALVREOPKDFVLONHNIRSNLERIFAKAPEPW 180
 DB 121 RSARGGQGSANDSYAALNAGSVQSAALVREOPKDFVLONHNIRSNLERIFAKAPEPW 180
 QY 181 VPPFOVSSFTNVDEMQEMADNYFGTGDAAAPPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
 DB 181 VPPFOVSSFTNVDEMQEMADNYFGTGDAAAPPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
 QY 241 LSGHLDPNRGRVPSNDVQVNVIDIAHYLTKLKWKEKLLGAQKQWQSNCKYKGRVQIKGCI 300
 DB 241 LSGHLDPNRGRVPSNDVQVNVIDIAHYLTKLKWKEKLLGAQKQWQSNCKYKGRVQIKGCI 300
 QY 301 PAIVLCNPGSGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYOESTQASOETGN 358
 DB 301 PAIVLCNPGSGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYOESTQASOEGH 358

RESULT 6
 Q7HTT9 PRELIMINARY; PRT; 361 AA.
 ID Q7HTT9
 AC Q7HTT9;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Replicase.
 GN Name=AC1;
 OS Tomato mottle Taino virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.

OX NCBI_TaxID=223358;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hernandez L.;
 RT "Caracterizaci3n molecular de geminivirus en papa (Solanium tuberosum L.)";
 RL Thesis (2000), Department of Biology, Universidad de La Habana, Ciudad de La Habana, Cuba.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Cordero M., Ramos P.L., Hernandez L., Fernandez A.I., Echemendia A.L., Peral R., Gonzalez G., Garcia D., Valdes S., Estevez A., Hernandez K.;
 RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF563919; CAD91703.1; -
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR InterPro; IPR001191; Gemini_AL1.
 DR Pfam; PF00799; Gemini_AL1.
 DR Prodom; PD000736; Gemini_AL1; 1.
 DR PRODOM; PD000736; Gemini_AL1; 1.
 SQ SEQUENCE 361 AA; 40735 MW; 78E289146A769404 CRC64;

Query Match 89.3%; Score 1731; DB 2; Length 361;
 Best Local Similarity 88.3%; Pred. No. 8e-127;
 Matches 316; Conservative 23; Mismatches 19; Indels 0; Gaps 0;

QY 1 MPPPKFRVQSKNYFLTYPCQSLSKERALSQLQNLNTPVKKFKIKICREIHENGEPHLHY 60
 DB 1 MPRKGSFSVAKNYFLTYPCQSLSKERALSQLQNLNTPVKKFKIKICREIHENGEPHLHY 60
 QY 61 LVQEGKYCTNNRFFDLVSPTRSAHFHPIIQAKSSDVKSYIDKQDITLWGDIFQIDG 120
 DB 61 LVQEGKYCTNNRFFDLVSPTRSAHFHPIIQAKSSDVKSYIDKQDITLWGDIFQIDG 120
 QY 121 RSRAGGQOSANDSYAKALNGVQSALAVLREBPQDFVLQNNHNRISNLERIFAKADEPW 180
 DB 121 RSRAGGQOSANDSYAKALNGVQSALAVLREBPQDFVLQNNHNRISNLERIFAKADEPW 180
 QY 121 RSRAGGQOSANDSYAKALNGVQSALAVLREBPQDFVLQNNHNRISNLERIFAKADEPW 180
 DB 121 RSRAGGQOSANDSYAKALNGVQSALAVLREBPQDFVLQNNHNRISNLERIFAKADEPW 180
 QY 181 VPPFOVSSFTNVDEQEMADNYFGTGDAAFPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
 DB 181 VPPPLSSFTNVDEQEMADNYFGAGSARPRPMSIVIEGDSRTGKTMMARALGPHNY 240
 QY 241 LSGHLDNNGVFNVDVQYNYIDIAPIHYLKLKHWKELGAKQWQSNCKYKGPQVQIKGI 300
 DB 241 LSGHLDNNTVYSNDVQYNYIDIAPIHYLKLKHWKELGAKQWQSNCKYKGPQVQIKGI 300
 QY 301 PAIVLCNPGGASGYKEFLDKAENTGLKNWTKNAIFITLPAIYQESTQASQETGNOK 358
 DB 301 PAIVLCNPGGASGYKDFLSKDENTSLRDWTKNAIFITLPAIYQESTQASQETGNOK 358

RESULT 7

ID 036624 PRELIMINARY; PRT; 361 AA.
 AC 036624;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Replication associated protein.
 OS Tomato mottle Taino virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=223358;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ramos P.L., Guerra O., Peral P., Oramas P., Guevara R.G., Rivera-Bustamante R.;
 RT "Taino tomato mottle virus, a new bipartite geminivirus from Cuba."; Plant Dis. 0:0-0(1997).
 CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
 DR EMBL; AF012300; AAO09668.1; -
 DR HSSP; P27260; ILST.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR001191; Gemini_AL1.

DR InterPro; IPR001301; Gemini_AL1_CLV.
 DR Pfam; PF00799; Gemini_AL1; 1.
 DR PRINTS; PR00227; GEMCOATL1.
 DR PRINTS; PR00228; GEMCOATCLV1.
 DR Prodom; PD000736; Gemini_AL1; 1.
 DR PRODOM; PD000736; Gemini_AL1; 1.
 SQ SEQUENCE 361 AA; 40722 MW; 3D43D231F8CC7FB5 CRC64;

Query Match 88.8%; Score 1722; DB 2; Length 361;
 Best Local Similarity 87.7%; Pred. No. 4.1e-126;
 Matches 314; Conservative 24; Mismatches 20; Indels 0; Gaps 0;

QY 1 MPPPKFRVQSKNYFLTYPCQSLSKERALSQLQNLNTPVKKFKIKICREIHENGEPHLHY 60
 DB 1 MPRKGSFSVAKNYFLTYPCQSLSKERALSQLQNLNTPVKKFKIKICREIHENGEPHLHY 60
 QY 61 LVQEGKYCTNNRFFDLVSPTRSAHFHPIIQAKSSDVKSYIDKQDITLWGDIFQIDG 120
 DB 61 LVQEGKYCTNNRFFDLVSPTRSAHFHPIIQAKSSDVKSYIDKQDITLWGDIFQIDG 120
 QY 121 RSRAGGQOSANDSYAKALNGVQSALAVLREBPQDFVLQNNHNRISNLERIFAKADEPW 180
 DB 121 RSRAGGQOSANDSYAKALNGVQSALAVLREBPQDFVLQNNHNRISNLERIFAKADEPW 180
 QY 181 VPPFOVSSFTNVDEQEMADNYFGTGDAAFPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
 DB 181 VPPPLSSFTNVDEQEMADNYFGAGSARPRPMSIVIEGDSRTGKTMMARALGPHNY 240
 QY 241 LSGHLDNNGVFNVDVQYNYIDIAPIHYLKLKHWKELGAKQWQSNCKYKGPQVQIKGI 300
 DB 241 LSGHLDNNTVYSNDVQYNYIDIAPIHYLKLKHWKELGAKQWQSNCKYKGPQVQIKGI 300
 QY 301 PAIVLCNPGGASGYKEFLDKAENTGLKNWTKNAIFITLPAIYQESTQASQETGNOK 358
 DB 301 PAIVLCNPGGASGYKDFLSKDENTSLRDWTKNAIFITLPAIYQESTQASQETGNOK 358

RESULT 8

ID 093051 PRELIMINARY; PRT; 361 AA.
 AC 093051;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Replication initiator protein.
 GN Name=AC1;
 OS Chino del tomate virus-[H8].
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=222454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Brown J.K., Nelson M.R.;
 RT "Transmission, host range, and virus-vector relationships of chino del tomate virus, a whitefly-transmitted geminivirus from Sinaloa, Mexico."; Plant Dis. 72:866-869(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Brown J.K., Ostrow K.M., Idris A.M., Stenger D.C.;
 RT "Chino del tomate virus: Relationships to other begomoviruses and the identification of A component variants that affect symptom expression."; Phytopathology 90:546-552(2000).
 CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
 DR EMBL; AF226664; AAF36703.1; -
 DR HSSP; P27260; ILST.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR001191; Gemini_AL1.
 DR InterPro; IPR001301; Gemini_AL1_CLV.
 DR Pfam; PF00799; Gemini_AL1; 1.
 DR PRINTS; PR00227; GEMCOATL1.
 DR PRINTS; PR00228; GEMCOATCLV1.
 DR Prodom; PD000736; Gemini_AL1; 1.

SEQUENCE 361 AA; 40970 MW; 9AF6F3865E1C2B822 CRC64;
Query Match 88.4%; Score 1715; DB 2; Length 361;
Best Local Similarity 87.2%; Pred. No. 1.4e-125;
Matches 312; Conservative 26; Mismatches 20; Indels 0; Gaps 0;
QY 1 MPPPKFRVQSKNYFLTYPCQCSLSKEBALSQLONTLPVNNKFIKICREIHENGEBPHLHV 60
DB 1 MPPPKFRVQSKNYFLTYPCQCSLSKEBALSQLONTLPVNNKFIKICREIHENGEBPHLHV 60
QY 61 LVQFEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVYSYIDKDGDTIEMGDFOIDG 120
DB 61 LVQFEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVYSYIDKDGDTIEMGDFOIDG 120
QY 121 RSARGGQQSANDSYAKALNAGSYQALAVLREBPQDPVYLQNNIRNSMERIPAKAPEPW 180
DB 121 RSARGGQQSANDSYAKALNAGSYQALAVLREBPQDPVYLQNNIRNSMERIPAKAPEPW 180
QY 181 VPPFQVSSFTNVDEQEWADNFGTGDAAAPRPPVSIIVEGSRGTGTMARALGPBNY 240
DB 181 VPPFQVSSFTNVDEQEWADNFGTGDAAAPRPPVSIIVEGSRGTGTMARALGPBNY 240
QY 241 LSGHLPNGRVFNSNDVQYNNVDDIAPHYLKLMKMKELGAQKQWQSNCKYKGFVQIKGKI 300
DB 241 LSGHLPNGRVFNSNDVQYNNVDDIAPHYLKLMKMKELGAQKQWQSNCKYKGFVQIKGKI 300
QY 301 PAIVLCNPGSGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQSTQASQETGNQK 358
DB 301 PAIVLCNPGSGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQSTQASQETGNQK 358
RESULT 9
Q96612 PRELIMINARY; PRT; 361 AA.
AC Q96612; (T-EMBLrel. 02, Created)
DT 01-FEB-1997 (T-EMBLrel. 02, Last sequence update)
DT 01-FEB-1997 (T-EMBLrel. 26, Last annotation update)
DE AC1 protein.
GN Name=AC1;
OS Abutilon mosaic virus-HW.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=222059;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Hawaii;
RT "Complete nucleotide sequence of a non-vector transmissible strain of
abutilon mosaic geminivirus in Hawaii."
RL Phytopathology 86:608-613 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=Hawaii;
RT Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
EMBL: U51137; AAB18173.1; -.
DR HSSP: P27260; 1L5I.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR001191; Gemin_ALI.
DR InterPro: IPR001301; Gemin_ALI_CLV.
DR Pfam: PF00799; Gemin_ALI.1.
DR PRINTS: PR00227; GEMCOATL1.
DR PRINTS: PR00228; GEMCOATL1.
DR PRODOM: PD000736; Gemin_ALI.1.
SQ SEQUENCE 361 AA; 40886 MW; 034D5A7608253CDC CRC64;
Query Match 88.2%; Score 1711; DB 2; Length 361;
Best Local Similarity 86.9%; Pred. No. 2.9e-125;
Matches 313; Conservative 26; Mismatches 21; Indels 0; Gaps 0;
QY 1 MPPPKFRVQSKNYFLTYPCQCSLSKEBALSQLONTLPVNNKFIKICREIHENGEBPHLHV 60

DB 1 MPPPKFRVQSKNYFLTYPCQCSLSKEBALSQLONTLPVNNKFIKICREIHENGEBPHLHV 60
QY 61 LVQFEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVYSYIDKDGDTIEMGDFOIDG 120
DB 61 LVQFEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVYSYIDKDGDTIEMGDFOIDG 120
QY 121 RSARGGQQSANDSYAKALNAGSYQALAVLREBPQDPVYLQNNIRNSMERIPAKAPEPW 180
DB 121 RSARGGQQSANDSYAKALNAGSYQALAVLREBPQDPVYLQNNIRNSMERIPAKAPEPW 180
QY 181 VPPFQVSSFTNVDEQEWADNFGTGDAAAPRPPVSIIVEGSRGTGTMARALGPBNY 240
DB 181 VPPFQVSSFTNVDEQEWADNFGTGDAAAPRPPVSIIVEGSRGTGTMARALGPBNY 240
QY 241 LSGHLPNGRVFNSNDVQYNNVDDIAPHYLKLMKMKELGAQKQWQSNCKYKGFVQIKGKI 300
DB 241 LSGHLPNGRVFNSNDVQYNNVDDIAPHYLKLMKMKELGAQKQWQSNCKYKGFVQIKGKI 300
QY 301 PAIVLCNPGSGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQSTQASQETGNQK 360
DB 301 PAIVLCNPGSGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQSTQASQETGNQK 360
RESULT 10
Q9J049 PRELIMINARY; PRT; 361 AA.
AC Q9J049; (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (T-EMBLrel. 26, Last annotation update)
DE Replication initiator protein.
GN Name=AC1;
OS Chino del tomate virus-[H6].
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=222453;
RN [1]
RP SEQUENCE FROM N.A.
RA Brown J.K., Nelson M.R.;
RT "Transmission, host range, and virus-vector relationships of chino del
tomate virus, a whitefly-transmitted geminivirus from Sinaloa,
Mexico."
RL Plant Dis. 72:866-869 (1988).
RN [2]
RP SEQUENCE FROM N.A.
RA Brown J.K., Ostrow K.M., Idris A.M., Stenger D.C.;
RT "Chino del tomate virus: relationships to other begomoviruses and the
identification of A component variants that affect symptom
expression."
RL Phytopathology 90:546-552 (2000).
CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
EMBL: AF226665; AAF36708.1; -.
DR HSSP: P27260; 1L5I.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR001191; Gemin_ALI.
DR InterPro: IPR001301; Gemin_ALI_CLV.
DR Pfam: PF00799; Gemin_ALI.1.
DR PRINTS: PR00227; GEMCOATL1.
DR PRINTS: PR00228; GEMCOATL1.
DR PRODOM: PD000736; Gemin_ALI.1.
SQ SEQUENCE 361 AA; 40928 MW; 85B43340272A8E10 CRC64;
Query Match 88.2%; Score 1710; DB 2; Length 361;
Best Local Similarity 86.6%; Pred. No. 3.5e-125;
Matches 310; Conservative 27; Mismatches 21; Indels 0; Gaps 0;
QY 1 MPPPKFRVQSKNYFLTYPCQCSLSKEBALSQLONTLPVNNKFIKICREIHENGEBPHLHV 60
DB 1 MPPPKFRVQSKNYFLTYPCQCSLSKEBALSQLONTLPVNNKFIKICREIHENGEBPHLHV 60
QY 61 LVQFEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVYSYIDKDGDTIEMGDFOIDG 120
DB 61 LVQFEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVYSYIDKDGDTIEMGDFOIDG 120

```
Db      61 LIQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQGAKESSDVYSYIDKGDITLWGEFQIDG 120
Qy      121 RSARGGQGSANDSYAKALNNGSVQSLAVLREBPCKPVLQNNIRISNLERIPAKAPEPW 180
Db      121 RSARGGQGSANDSYAKALNNGSVQSLAVLREBPCKPVLQNNIRISNLERIPAKAPEPW 180
Qy      181 VPPFQVSSFTNNVEDQEMADNYFGTGDAAFPDRPSVSIIEGDSRTGKTMMARALGPHNY 240
Db      181 VPPFQVSSFTNNVEDQEMADNYFGTGDAAFPDRPSVSIIEGDSRTGKTMMARALGPHNY 240
Qy      241 LSGHLDENGKRVFNSDVQYNNVIDIAPHYLKLGKMKELGAKQKQMSCKTGKPVQIKGI 300
Db      241 LSGHLDENGKRVFNSDVQYNNVIDIAPHYLKLGKMKELGAKQKQMSCKTGKPVQIKGI 300
Qy      301 PAIVLCNPGGASGYKEFLDKAENTGLKNWTTIKNAIFITLTAPLYQESTQASQETGNOK 358
Db      301 PAIVLCNPGGASGYKEFLDKAENTGLKNWTTIKNAIFITLTAPLYQESTQASQETGNOK 358
```

RESULT 11

```
PRELIMINARY; PRT; 361 AA.
ID      P89127
AC      P89127;
DT      01-MAY-1997 (TrEMBLrel. 03, Created)
DT      01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Acl protein.
GN      Name=Acl;
OS      Sida yellow vein virus.
OC      Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NCBI TaxID=223321;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Honduras;
RX      MEDLINE=98007646; PubMed=9349490;
RA      Frieschmuth T., Engel M., Lauster S., Jeske H.;
RT      "Nucleotide sequence evidence for the occurrence of three distinct
RT      whitefly-transmitted, Sida-infecting bipartite geminiviruses in
RT      Central America.";
RL      J. Gen. Virol. 78:2675-2682(1997).
CC      -1- SIMILARITY: Belongs to the geminiviruses Acl protein family.
DR      EMBL; Y11099; CAU71980.1; -.
DR      HSSP; P27260; ILS1.
DR      GO; GO:0019028; C:Viral capsid; IEA.
DR      GO; GO:0005198; F:Structural molecule activity; IEA.
DR      InterPro; IPR001191; Gemin1_Acl.
DR      InterPro; IPR001301; Gemin1_Acl_CTV.
DR      Pfam; Pf00799; Gemin1_Acl.1.
DR      PRINTS; PR00227; GEMCOATL1.
DR      PRINTS; PR00228; GEMCOATL1.
DR      ProDom; PD000736; Gemin1_Acl.1.
SQ      SEQUENCE 361 AA; 40956 MW; DF473608465F2987 CRC64;
```

Query Match 87.2%; Score 1690; DB 2; Length 361;
Best Local Similarity 85.8%; Pred. No. 1.3e-123;
Matches 307; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

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Qy      1 MPPPKKRVQSKNYFLTYPCSLSKKEALSQQLNTLPVKKKFKIKRELHENGEPHLAV 60
Db      1 MPPPKKRVQSKNYFLTYPCSLSKKEALSQQLNTLPVKKKFKIKRELHENGEPHLAV 60
Qy      61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQGAKESSDVYSYIDKGDITLWGEFQIDG 120
Db      61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQGAKESSDVYSYIDKGDITLWGEFQIDG 120
Qy      121 RSARGGQGSANDSYAKALNNGSVQSLAVLREBPCKPVLQNNIRISNLERIPAKAPEPW 180
Db      121 RSARGGQGSANDSYAKALNNGSVQSLAVLREBPCKPVLQNNIRISNLERIPAKAPEPW 180
Qy      181 VPPFQVSSFTNNVEDQEMADNYFGTGDAAFPDRPSVSIIEGDSRTGKTMMARALGPHNY 240
Db      181 VPPFQVSSFTNNVEDQEMADNYFGTGDAAFPDRPSVSIIEGDSRTGKTMMARALGPHNY 240
Qy      301 PAIVLCNPGGASGYKEFLDKAENTGLKNWTTIKNAIFITLTAPLYQESTQASQETGNOK 358
Db      301 PAIVLCNPGGASGYKEFLDKAENTGLKNWTTIKNAIFITLTAPLYQESTQASQETGNOK 358
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```
Qy      241 LSGHLDENGKRVFNSDVQYNNVIDIAPHYLKLGKMKELGAKQKQMSCKTGKPVQIKGI 300
Db      241 LSGHLDENGKRVFNSDVQYNNVIDIAPHYLKLGKMKELGAKQKQMSCKTGKPVQIKGI 300
Qy      301 PAIVLCNPGGASGYKEFLDKAENTGLKNWTTIKNAIFITLTAPLYQESTQASQETGNOK 358
Db      301 PAIVLCNPGGASGYKEFLDKAENTGLKNWTTIKNAIFITLTAPLYQESTQASQETGNOK 358
```

RESULT 12

```
PRELIMINARY; PRT; 361 AA.
ID      Q8JUV1
AC      Q8JUV1;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Replication associated protein.
GN      Name=Acl;
OS      Tobacco leaf rugose virus.
OC      Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NCBI TaxID=196691;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Dominguez M., Ramos P.L., Echmendia A.L., Crespo J., Peral R.,
RA      Pujol M., Andino V., Borroto C.;
RT      Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: Belongs to the geminiviruses Acl protein family.
DR      EMBL; AJ488768; CAD32806.1; -.
DR      HSSP; P27260; ILS1.
DR      GO; GO:0019028; C:Viral capsid; IEA.
DR      GO; GO:0005198; F:Structural molecule activity; IEA.
DR      InterPro; IPR001191; Gemin1_Acl.
DR      InterPro; IPR001301; Gemin1_Acl_CTV.
DR      Pfam; Pf00799; Gemin1_Acl.1.
DR      PRINTS; PR00227; GEMCOATL1.
DR      PRINTS; PR00228; GEMCOATL1.
DR      ProDom; PD000736; Gemin1_Acl.1.
SQ      SEQUENCE 361 AA; 41036 MW; 1291C2DC119EABAI CRC64;
```

Query Match 87.1%; Score 1689; DB 2; Length 361;
Best Local Similarity 86.1%; Pred. No. 1.5e-123;
Matches 311; Conservative 24; Mismatches 24; Indels 2; Gaps 2;

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Qy      1 MPPPKKRVQSKNYFLTYPCSLSKKEALSQQLNTLPVKKKFKIKRELHENGEPHLAV 60
Db      1 MPPPKKRVQSKNYFLTYPCSLSKKEALSQQLNTLPVKKKFKIKRELHENGEPHLAV 60
Qy      61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQGAKESSDVYSYIDKGDITLWGEFQIDG 120
Db      61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQGAKESSDVYSYIDKGDITLWGEFQIDG 120
Qy      121 RSARGGQGSANDSYAKALNNGSVQSLAVLREBPCKPVLQNNIRISNLERIPAKAPEPW 180
Db      121 RSARGGQGSANDSYAKALNNGSVQSLAVLREBPCKPVLQNNIRISNLERIPAKAPEPW 180
Qy      181 VPPFQVSSFTNNVEDQEMADNYFGTGDAAFPDRPSVSIIEGDSRTGKTMMARALGPHNY 240
Db      181 VPPFQVSSFTNNVEDQEMADNYFGTGDAAFPDRPSVSIIEGDSRTGKTMMARALGPHNY 240
Qy      301 PAIVLCNPGGASGYKEFLDKAENTGLKNWTTIKNAIFITLTAPLYQESTQASQETGNOK 358
Db      301 PAIVLCNPGGASGYKEFLDKAENTGLKNWTTIKNAIFITLTAPLYQESTQASQETGNOK 358
```

RESULT 13

```
Q67558
ID Q67558 PRELIMINARY; PRT; 361 AA.
AC Q67558;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Replicative protein.
GN Name=AL1;
OS Bean dwarf mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=10838;
[1]
RN
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RT "Cloning of the complete DNA genomes of four bean-infecting
RT geminiviruses and determining their infectivity by electric discharge
RT particle acceleration.";
RL Phytopathology 81:980-985(1991).
[2]
RN
RP SEQUENCE FROM N.A.
RA Hidayat S.H., Gilbertson R.L., Hanson S.F., Morales F.J.,
RA Ahlquist P.G., Russell D.R., Maxwell D.P.;
RL Submitted (May-1992) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
DR EMBL; M88179; AAC32402.1; -.
DR HSSP; P27260; 1L5T.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001191; Gemin1 AL1.
DR InterPro; IPR001301; Gemin1 AL1_CLV.
DR Pfam; PF00799; Gemin1 AL1.
DR PRINTS; PR00227; GEMCOATL1.
DR PRINTS; PR00228; GEMCOATL1.
DR PRODOM; PD000736; Gemin1 AL1.
SQ
SEQUENCE 361 AA; 40733 MW; A26939B1BEF923A8 CRC64;

Query Match 85.8%; Score 1664; DB 2; Length 361;
Best Local Similarity 83.2%; Pred. No. 1.4e-121;
Matches 298; Conservative 35; Mismatches 25; Indels 0; Gaps 0;

QY 1 MPPKPRVQSKNYFLTYPCQSLSKERALSQLQNTLPVNNKFKIKRELHENGEPHLAV 60
DB 1 MPPKPRVQSKNYFLTYPCQSLSKERALSQLQNTLPVNNKFKIKRELHENGEPHLAV 60
QY 61 LVOPEGKYQCTNNRFPDLVSPTRSAHFHPNIQGAKSSSDVKSVIDKDGDTIEWGDFQIDG 120
DB 61 LVOPEGKYQCTNNRFPDLVSPTRSAHFHPNIQGAKSSSDVKSVIDKDGDTIEWGDFQIDG 120
QY 121 RSARGGQOSANDSYAKALNAGVQSALAVIREOPKDFVLQNNHNSLERTFAKAPBPW 180
DB 121 RSARGGQOSANDSYAKALNAGVQSALAVIREOPKDFVLQNNHNSLERTFAKAPBPW 180
QY 121 RSARGGQOSANDSYAKALNAGVQSALAVIREOPKDFVLQNNHNSLERTFAKAPBPW 180
DB 121 RSARGGQOSANDSYAKALNAGVQSALAVIREOPKDFVLQNNHNSLERTFAKAPBPW 180
QY 181 VPPFOVSSFTNVDEQEMADNYFGTGDAPRDPVSIIEGDSRTGKTMARALGPHNY 240
DB 181 VPPFOVSSFTNVDEQEMADNYFGTGDAPRDPVSIIEGDSRTGKTMARALGPHNY 240
QY 241 LSGHLDNFNGRVPSNDVQYNNIDIAAPHYLKLGKMKELIGAQKQWQSNCKYKGPVQIKGKI 300
DB 241 LSGHLDNFNGRVPSNDVQYNNIDIAAPHYLKLGKMKELIGAQKQWQSNCKYKGPVQIKGKI 300
QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTKIKNAIFITLTAPLYQESTQASQETGNQK 358
DB 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTKIKNAIFITLTAPLYQESTQASQETGNQK 358

RESULT 14
ID Q71205 PRELIMINARY; PRT; 350 AA.
AC Q71205;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
```

```
DE Replication-associated protein.
GN Name=AC1;
OS Potato yellow mosaic Trinidad virus-[Trinidad & Tobago].
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=223309;
[1]
RN
RP SEQUENCE FROM N.A.
RA Humataran P., Padidam M., Phelps R.H., Beachy R.N., Fauquet C.M.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
DR EMBL; AF039031; AAC09254.1; -.
DR HSSP; P27260; 1L5T.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001191; Gemin1 AL1.
DR InterPro; IPR001301; Gemin1 AL1_CLV.
DR Pfam; PF00799; Gemin1 AL1.
DR PRINTS; PR00227; GEMCOATL1.
DR PRINTS; PR00228; GEMCOATL1.
DR PRODOM; PD000736; Gemin1 AL1.
SQ
SEQUENCE 350 AA; 39567 MW; A08E3B3BFLA068FD CRC64;

Query Match 85.2%; Score 1652; DB 2; Length 350;
Best Local Similarity 84.5%; Pred. No. 1.1e-120;
Matches 295; Conservative 27; Mismatches 27; Indels 0; Gaps 0;

QY 3 PPKPRVQSKNYFLTYPCQSLSKERALSQLQNTLPVNNKFKIKRELHENGEPHLAV 62
DB 2 PPKPRVQSKNYFLTYPCQSLSKERALSQLQNTLPVNNKFKIKRELHENGEPHLAV 61
QY 63 QPEGKYQCTNNRFPDLVSPTRSAHFHPNIQGAKSSSDVKSVIDKDGDTIEWGDFQIDG 122
DB 62 QPEGKYQCTNNRFPDLVSPTRSAHFHPNIQGAKSSSDVKSVIDKDGDTIEWGDFQIDG 121
QY 123 ARGGQOSANDSYAKALNAGVQSALAVIREOPKDFVLQNNHNSLERTFAKAPBPW 182
DB 122 ARGGQOSANDSYAKALNAGVQSALAVIREOPKDFVLQNNHNSLERTFAKAPBPW 181
QY 183 PFOVSSFTNVDEQEMADNYFGTGDAPRDPVSIIEGDSRTGKTMARALGPHNY 242
DB 182 PFOVSSFTNVDEQEMADNYFGTGDAPRDPVSIIEGDSRTGKTMARALGPHNY 241
QY 243 GHLDNFNGRVPSNDVQYNNIDIAAPHYLKLGKMKELIGAQKQWQSNCKYKGPVQIKGIPA 302
DB 242 GHLDNFNGRVPSNDVQYNNIDIAAPHYLKLGKMKELIGAQKQWQSNCKYKGPVQIKGIPA 301
QY 303 IVLCNPGEGASYKEFLDKAENTGLKNWTKIKNAIFITLTAPLYQESTQAS 351
DB 302 IVLCNPGEGASYKEFLDKAENTGLKNWTKIKNAIFITLTAPLYQESTQAS 350

RESULT 15
ID P89122 PRELIMINARY; PRT; 361 AA.
AC P89122;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AC1 protein.
GN Name=AC1;
OS Sida golden mosaic Honduras virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=223316;
[1]
RN
RP SEQUENCE FROM N.A.
RA STRAIN=Honduras;
RA MEDLINE=98007646; PubMed=9349490;
RA Frischmuth T., Engel M., Lauster S., Jeske H.;
RT "Nucleotide sequence evidence for the occurrence of three distinct
RT whitefly-transmitted, Sida-infecting bipartite geminiviruses in
RT Central America.";
RL J. Gen. Virol. 78:2675-2682(1997).
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CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
DR EMBL: Y11097; CAA71973.1; -.
DR HSSP: P27260; 1L5I.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR01191; Gemini_AL1.
DR InterPro: IPR01301; Gemini_AL1_CLV.
DR Pfam: PF00799; Gemini_AL1_1.
DR PRINTS: PR00227; GEMCOTALI.
DR PRINTS: PR00228; GEMCONTCLV1.
DR PRODOM: PD000736; Gemini_AL1; 1.
DR SEQUENCE 361 AA; 4137 MW; 5BE4C17CE1C7E4DF CRC64;

Query March 84.6% Score 1640; DB 2; Length 361;

Best Local Similarity 82.7%; Pred. No. 1e-119; Mismatches 33; Indels 0; Gaps 0;

Matches 296; Conservative 29; Mismatches 33; Indels 0; Gaps 0;

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QY 1 MPPKRRVOSKNYFLTYPOCSLSKEEALSQLQNLNTPVNNKFTIKICRELHENGEPHLHV 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MPPKRRVNSKNYFLTYPOCSLTKEALSQFTLTTPVNNKFTIKISRDKHENGEPHQHV 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQGAKSSDVKSYTDKDGDTIEWGDFQIDG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LIOPEGKYQCTNNRFPDLVSPTRSAHFHPNIQGAKSSDVKSYTDKDGDTIEWGDFQIDG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 RSARGGQOSANDSYAKALNAGSVOSALAVLREOQPKDFVLQNNHNRSLERIFAKAPEPW 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 RSARGGQOTANDTYAKALNATCAEALRIIREQPGHFLOHNLVANATKIFQKAPPEPW 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 181 VPPQVSSFTNVPEQEMADNYPFGTDAAPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 APPPLSSFTNVPEQEMADEYFGRGSAARPPDRPMSLIIVEGDSRTGKTMMARALGPHNY 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 241 LSGHLDENGSRVSDVQYNYVDIAPHYLKLKHWKELLGAQKWQSNCKYGPVQIKGI 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 LSGHLDENPRVSNVEYNYVDVAPHYLKLKHWKELLGAQKWQSNCKYGPVQIKGI 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNMTIKNAIFITLTAPLYQESTQASQETGNOK 358
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 PSTVLCNPGEGASYKDFLDKEENASLNMTIKNAIFITLTALYQDSTQASQEBVHOE 358
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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Search completed: December 3, 2004, 15:00:48
Job time : 195 secs